

# SEQUENCE LISTING

<110> Sim, Gek-Kee  
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<120> CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
ACID MOLECULES, AND USES THEREOF

<130> IM-2-C2

<140> not yet assigned

<141> 1999-12-01

<150> 09/322,409

<151> 1999-05-28

<150> 60/087,306

<151> 1998-05-29

<160> 174

<170> PatentIn Ver. 2.0

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<212> DNA

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Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys  
25 30 35

atg ttg aac atc ctc aca gcg aga aac gac tcg tgc atg gag ctg act 198

Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr  
 40 45 50

gtc aag gac gtc ttc act gct cca aag aac aca agc gat aag gaa atc 246  
 Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile  
 55 60 65

ttc tgc aga gct gct act gta ctg cgg cag atc tat aca cac aac tgc 294  
 Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys  
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tcc aac aga tat ctc aga gga ctc tac agg aac ctc agc agc atg gca 342  
 Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala  
 85 90 95 100

aac aag acc tgt tct atg aat gaa atc aag aag agt aca ctg aaa gac 390  
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 105 110 115

ttc ttg gaa agg cta aaa gtg atc atg cag aag aaa tac tac agg cat 438  
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Glu Ile Ile Lys Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys  
 35 40 45

Met Glu Leu Thr Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser  
 50 55 60

Asp Lys Glu Ile Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr  
 65 70 75 80

661027: 4434560

Thr His Asn Cys Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu  
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Ser Ser Met Ala Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser  
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aagaacacaa gcgataagga aatcttctgc agagctgcta ctgtactgcg gcagatctat 240  
acacacaact gctccaacag atatctcaga ggactctaca ggaacctcag cagcatggca 300  
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Trp Ser Pro Thr Ala Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly	
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ctc cgc ggg acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc	151
Leu Arg Gly Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser	
25 30 35	
acc ttc gcg gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac	199
Thr Phe Ala Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp	
40 45 50 55	
tat cca gtc act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg	247
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly	
60 65 70	
gcg ttc tgg cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag	295
Ala Phe Trp Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln	
75 80 85	
gct gtg gct gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg	343
Ala Val Ala Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr	
90 95 100	
gag ata cac ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt	391
Glu Ile His Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys	
105 110 115	
ctt cgc ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc	439
Leu Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser	
120 125 130 135	
cag cag ctg gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc	487
Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser	
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ggg tgc ctg gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc	535
Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro	
155 160 165	
cca agg agc ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag	583
Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln	
170 175 180	
gca cct cgg ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg	631
Ala Pro Arg Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu	
185 190 195	

atg tcc act gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg 679  
Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg  
200 205 210 215

tca ccc tac cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc 727  
Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser  
220 225 230

cat ctg ccc gag gac aca gag ctg gga cct gga ggg agt cag cta gag 775  
His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu  
235 240 245

act ggt ccc ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga 823  
Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly  
250 255 260

tca agg caa cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca 871  
Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro  
265 270 275

cct ctc ccc ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata 916  
Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile  
280 285 290

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Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu  
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
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Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln  
65 70 75 80

Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile  
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Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala  
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Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
115 120 125

His Leu Leu Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp  
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Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro  
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Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala  
165 170 175

Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu  
180 185 190

Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp  
195 200 205

Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr  
210 215 220

Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly  
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Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala  
245 250 255

Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro  
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<212> DNA

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 <223> Description of Artificial Sequence: Synthetic  
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<210> 13  
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<210> 14

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<211> 18

<212> DNA

<213> Artificial Sequence

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ctc aca gcg aga aac gac tcg tgc atg gag ctg act gtc aag gac gtc 96  
Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr Val Lys Asp Val  
20 25 30

ttc act gct cca aag aac aca agc gat aag gaa atc ttc tgc aga gct 144  
Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala  
35 40 45

gct act gta ctg cgg cag atc tat aca cac aac tgc tcc aac aga tat 192

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr  
 50 55 60

ctc aga gga ctc tac agg aac ctc agc agc atg gca aac aag acc tgt 240  
 Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys  
 65 70 75 80

tct atg aat gaa atc aag aag agt aca ctg aaa gac ttc ttg gaa agg 288  
 Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg  
 85 90 95

cta aaa gtg atc atg cag aag aaa tac tac agg cat 324  
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 <212> PRT  
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Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala  
 35 40 45

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr  
 50 55 60

Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys  
 65 70 75 80

Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg  
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Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His  
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 agctctgcag aagatttctt tatcgcttgt gttctttgga gcagtgaaga cgtccttgac 240  
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 gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96  
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
 20 25 30  
 act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg 144  
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp  
 35 40 45  
 cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192  
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala  
 50 55 60  
 gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240  
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His  
 65 70 75 80  
 ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt ctt cgc ttc 288  
 Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe  
 85 90 95

gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc cag cag ctg	336
Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu	
100 105 110	
gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg	384
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu	
115 120 125	
gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc cca agg agc	432
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser	
130 135 140	
ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag gca cct cgg	480
Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg	
145 150 155 160	
ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act	528
Leu Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr	
165 170 175	
gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac	576
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr	
180 185 190	
cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc cat ctg ccc	624
Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro	
195 200 205	
gag gac aca gag ctg gga cct gga ggg agt cag cta gag act ggt ccc	672
Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro	
210 215 220	
ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga tca agg caa	720
Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln	
225 230 235 240	
cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca cct ctc ccc	768
Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro	
245 250 255	
ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata	804
Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile	
260 265	

<210> 23  
<211> 268

<212> PRT

<213> Canis familiaris

<400> 23

Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala  
1 5 10 15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp  
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala  
50 55 60

Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe  
85 90 95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu  
100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser  
130 135 140

Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg  
145 150 155 160

Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr  
165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr  
180 185 190

Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro  
195 200 205

Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro  
210 215 220

Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln  
225 230 235 240



Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro  
 245 250 255

Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile  
 260 265

<210> 24  
 <211> 804  
 <212> DNA  
 <213> Canis familiaris

<400> 24  
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 gtggtcgagg aagggaccag tctctagctg actccctcca ggtcccagct ctgtgtcctc 180  
 gggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tcccagggt agggtgacct 240  
 ccgccgccgc ctccctcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300  
 gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360  
 cagggccccg gggctccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420  
 caggcaccgc gagaaattcc tgcgggtgat ccagggttc agggcggcca gctgctggga 480  
 ggtgtcctgc aggaggtggg agatgttggg ctggacgaag cgaagacagc tggggagggg 540  
 ctggaaggca cagaaggtga caaagtgtat ctccgtgttg acagcctcca gcaggatttg 600  
 catttgggat ccagccacag cctggagccg caccatccag cgctgggcca ggaccaggcg 660  
 ccagaacgcc ccgcagagct cgtcgtcctg caggttggag gcgacagtga ctggatagtc 720  
 ctgaagcagg taatcagaca gcttgccgat ggtgaccgcg aaggtggagg agatggggct 780  
 gtggctgaag gagcagtcgg gggt 804

<210> 25  
 <211> 985  
 <212> DNA  
 <213> Canis familiaris

<220>

<221> CDS

<222> (74)..(901)

<400> 25

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gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gcc 109

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala

1

5

10

tcc ctg ttg ctg ctg ctg ctg ctc agc ccc ggc ctc cgc ggg acc ccc 157

Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro

15

20

25

gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg gtc acc 205

Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr

30

35

40

atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc act gtc 253

Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val

45

50

55

60

gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg cgc ctg 301

Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu

65

70

75

gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct gga tcc 349

Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser

80

85

90

caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac ttt gtc 397

Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val

95

100

105

acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc ctg aag 445

Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys

110

115

120

ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg cag tgt 493

Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys

125

130

135

140

cag ccc gac tcc tct aca ttg gtg ccc cca agg agc ccc ggg gcc ctg 541

Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu

145

150

155

gag gcc act gcc ttg cca gcc cct cag gca cct cgg ctg ctc ctc ctg 589

Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu  
160 165 170

ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act gcc tgg tgc ctg 637  
Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu  
175 180 185

cat tgg cga agg agg cgg cgg cgg agg tca ccc tac cct ggg gag cag 685  
His Trp Arg Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln  
190 195 200

agg aca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac aca gag 733  
Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu  
205 210 215 220

ctg gga cct gga ggg agt cag cta gag act ggt ccc ttc ctc gac cac 781  
Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His  
225 230 235

gca gcc ccg ctc gct ccc tcc cca gga tca agg caa cgc ccg ccc cca 829  
Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro  
240 245 250

acg ccc cca aag cca gcc cca gcc cca cct ctc ccc ctc tgt aca aag 877  
Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys  
255 260 265

tcc ttg ccc cca aga aat tgt ata taaatcatcc ttttctacca gcaaaaaaaaa 931  
Ser Leu Pro Pro Arg Asn Cys Ile  
270 275

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 985

<210> 26

<211> 276

&lt;212&gt; PRT

<213> Canis familiaris

<400> 26

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala Ser Leu Leu Leu  
1 5 10 15

Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro Asp Cys Ser Phe  
20 25 30

Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu  
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
50 55 60

Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln  
65 70 75 80

Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile  
85 90 95

Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala  
100 105 110

Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr  
115 120 125

Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser  
130 135 140

Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala  
145 150 155 160

Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu Pro  
165 170 175

Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg  
180 185 190

Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg  
195 200 205

Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly  
210 215 220

Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu  
225 230 235 240

Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys  
245 250 255

Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro  
260 265 270

Arg Asn Cys Ile  
275

<210> 27

<211> 985  
<212> DNA  
<213> Canis familiaris

<400> 27

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ggggagaggt ggggctgggg ctggccttgg gggcggttgg ggcgggctt gccttgatcc 180  
tggggagggg gcgagcgggg ctgcgtgggc gaggaaggga ccagtctcta gctgactccc 240  
tccaggtccc agctctgtgt cctcgggcag atggctccgc tcgctgggccc tcagtgtcct 300  
ctgctcccca gggtaggggtg acctccgcgc ccgcctcctt cgccaatgca ggcaccaggc 360  
agtggacatc agcaggagag ccacgggcag cagcagcagg aggagcagcc gaggtgcctg 420  
aggggctggc aaggcagtgg cctccagggc cccggggctc cttgggggca ccaatgtaga 480  
ggagtcgggc tgacactgca gctccaggca cccggagaaa ttcttgccgg tgatccaggg 540  
cttcagggcg gccagctgct gggaggtgtc ctggaaggca cagaagggtga caaagtgtat 600  
ctccgtgttg acagcctcca gcaggatttg catttgggat ccagccacag cctggagccg 660  
caccatccag cgctggggcca ggaccaggcg ccagaacgcc ccgcagagct cgtcgtcctg 720  
caggttgagg gcgacagtga ctggatagtc ctgaagcagg taatcagaca gcttgccgat 780  
ggtgaccgcg aaggtggagg agatggggct gtggctgaag gagcagtcgg ggggtcccgcg 840  
gaggccgggg ctgagcagca gcagcagcaa cagggaggca gttgggctcc aggctggcgc 900  
cagcactatc atctcggccg gaggccctc atgcctatgg tcagatcagg cttgccccag 960  
ctgggcgtgg aaggggccag gccgg 985

<210> 28  
<211> 828  
<212> DNA  
<213> Canis familiaris

<400> 28

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agccccggcc tccgcgggac ccccgactgc tccttcagcc acagccccat ctctccacc 120  
 ttgcgggtca ccatccgcaa gctgtctgat tacctgcttc aggactatcc agtcactgtc 180  
 gcctccaacc tgcaggacga cgagctctgc gggcggttct ggcgcttgt cctggcccag 240  
 cgctggatgg tgcggctcca ggctgtggct ggatcccaaa tgcaaatact gctggaggct 300  
 gtcaacacgg agatacactt tgtcaccttc tgtgccttcc aggacacctc ccagcagctg 360  
 gccgccctga agccctggat caccgcagg aatttctccg ggtgcctgga gctgcagtgt 420  
 cagcccgact cctctacatt ggtgccccca aggagccccg gggccctgga ggccactgcc 480  
 ttgccagccc ctccaggcacc tcggctgctc ctctgctgc tgcctgccgt ggctctctg 540  
 ctgatgtcca ctgcctgggtg cctgcattgg cgaaggaggc ggcgggcgag gtcaccctac 600  
 cctgggggagc agaggacact gagggccagc gagcggagcc atctgcccga ggacacagag 660  
 ctgggacctg gagggagtca gctagagact ggtcccttcc tcgaccacgc agccccgctc 720  
 gctccctccc caggatcaag gcaacgcccg ccccaaacgc ccccaaagcc agccccagcc 780  
 ccacctctcc ccctctgtac aaagtccttg ccccaagaa attgtata 828

<210> 29  
 <211> 828  
 <212> DNA  
 <213> Canis familiaris

<400> 29  
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 ctttgggggc gttgggggag ggcgttgctt tgatcctggg gagggagcga gcggggctgc 120  
 gtggctgagg aagggaccag tctctagctg actccctcca ggtcccagct ctgtgtctc 180  
 gggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tcccagggt agggtgacct 240  
 ccgccgccgc ctcttcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300  
 gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360  
 cagggccccg gggctccttg ggggcaccaa ttagaggag tcgggctgac actgcagctc 420  
 caggcaccgc gagaaattcc tgcgggtgat ccagggcttc agggcgcca gctgctggga 480

ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540  
 gatttgcatt tgggatccag ccacagcctg gagccgcacc atccagcgct gggccaggac 600  
 caggcgccag aacgccccgc agagctcgtc gtcctgcagg ttggaggcga cagtgactgg 660  
 atagtctga agcaggtaat cagacagctt gcggatgggt accgcgaagg tggaggagat 720  
 ggggctgtgg ctgaaggagc agtcgggggt cccgcggagg cgggggctga gcagcagcag 780  
 cagcaacagg gaggcagttg ggctccaggc tggcgccagc actatcat 828

<210> 30  
 <211> 750  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(750)

<400> 30  
 acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg 48  
 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala  
 1 5 10 15  
 gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96  
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
 20 25 30  
 act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg 144  
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp  
 35 40 45  
 cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192  
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala  
 50 55 60  
 gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240  
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His  
 65 70 75 80  
 ttt gtc acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc 288  
 Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala  
 85 90 95





15

Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile  
245 250

<210> 32  
 <211> 750  
 <212> DNA  
 <213> Canis familiaris

<400> 32  
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 gtggtcgagg aagggaaccag tctctagctg actccctcca ggtcccagct ctgtgtcctc 180  
 gggcagatgg ctccgctcgc tgggcctcag tgcctctgc tcccaggggt agggtgacct 240  
 ccgccgccgc ctcttcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300  
 gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360  
 cagggccccg gggctccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420  
 caggcaccgc gagaaattcc tgcgggtgat ccagggcctc agggcggcca gctgctggga 480  
 ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540  
 gatttgcat tgggatccag ccacagcctg gagccgcacc atccagcgct gggccaggac 600  
 caggcgccag aacgccccgc agagctcgtc gtcctgcagg ttggaggcga cagtgactgg 660  
 atagtcctga agcaggtaat cagacagctt gcggatgggt accgcgaagg tggaggagat 720  
 ggggctgtgg ctgaaggagc agtcgggggt 750

<210> 33  
 <211> 1019  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (74)..(166)

<400> 33  
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 gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gtg 109  
 Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val  
 1 5 10

cgt ata ccc ggg gga caa ggc ggg gga cag gca gag cgc tac cga gct 157  
 Arg Ile Pro Gly Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala  
           15                    20                    25

ggg cag agc tgagagagca gacggacaga ggccctccctg ttgctgctgc 206  
 Gly Gln Ser  
           30

tgctgctcag ccccggcctc cgcgggaccc ccgactgctc cttcagccac agccccatct 266

cctccacctt cgcggtcacc atccgcaagc tgtctgatta cctgcttcag gactatccag 326

tcactgtcgc ctccaacctg caggacgacg agctctgcgg ggcgttctgg cgcttggtcc 386

tggcccagcg ctggatggtg cggtccagg ctgtggctgg atcccaaagt caaatcctgc 446

tggaggctgt caacacggag atacactttg tcaccttctg tgccttccag gacacctccc 506

agcagctggc cgccctgaag ccctggatca cccgcaggaa tttctccggg tgcctggagc 566

tgcagtgtca gcccgactcc tctacattgg tgcccccaag gagccccggg gccctggagg 626

ccactgcctt gccagccctt caggcacctc ggctgctcct cctgctgctg ctgcccgtgg 686

ctctcctgct gatgtccact gcttgggtgcc tgcattggcg aaggaggcgg cggcggaggt 746

cacctaccc tggggagcag aggacactga ggcccagcga gcggagccat ctgcccagg 806

acacagagct gggacctgga gggagtcagc tagagactgg tcccttcctc gaccacgcag 866

ccccgctcgc tccctcccca ggatcaaggc aacgcccgcc cccaacgccc ccaaagccag 926

ccccagcccc acctctcccc ctctgtacaa agtccttgcc cccaagaaat tgtatataaa 986

tcctcctttt ctaccaaaaa aaaaaaaaaa aaa 1019

<210> 34

<211> 31

<212> PRT

<213> Canis familiaris

<400> 34

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val Arg Ile Pro Gly  
           1                    5                    10                    15

Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala Gly Gln Ser

CGT ATA CCC GGG GGA CAA GGC GGG GGA CAG GCA GAG CGC TAC CGA GCT

<210> 35  
 <211> 1019  
 <212> DNA  
 <213> Canis familiaris

<400> 35  
 tttttttttt ttttttttgg tagaaaagga tgatttatat acaatttctt gggggcaagg 60  
 actttgtaca gagggggaga ggtggggctg gggctggctt tgggggcgtt gggggcgggc 120  
 gttgccttga tcctggggag ggagcgagcg gggctgcgtg gtcgaggaag ggaccagtct 180  
 ctagctgact ccctccaggt ccagctctg tgcctcggg cagatggctc cgctcgctgg 240  
 gcctcagtgt cctctgctcc ccagggtagg gtgacctccg ccgccgcctc cttcgccaat 300  
 gcaggcacca ggcagtggac atcagcagga gagccacggg cagcagcagc aggaggagca 360  
 gccgaggtgc ctgaggggct ggcaaggcag tggcctccag ggccccgggg ctccttgggg 420  
 gcaccaatgt agaggagtcg ggctgacact gcagctccag gcacccggag aaattcctgc 480  
 gggatgatcca gggcttcagg gcggccagct gctgggaggt gtcctggaag gcacagaagg 540  
 tgacaaagtg tatctccgtg ttgacagcct ccagcaggat ttgcatttgg gatccagcca 600  
 cagcctggag ccgcaccatc cagcgtctgg ccaggaccag gcgccagaac gccccgcaga 660  
 gctcgtcgtc ctgcaggttg gaggcgacag tgactggata gtcctgaagc aggtaatcag 720  
 acagcttgcg gatggtgacc gcgaagggtg aggagatggg gctgtggctg aaggagcagt 780  
 cgggggtccc gcggaggccg gggctgagca gcagcagcag caacagggag gcctctgtcc 840  
 gtctgctctc tcagctctgc ccagctcggg agcgtctctg ctgtcccccg ccttgtcccc 900  
 cgggtatacg cacagttggg ctccaggctg gcgccagcac tatcatctcg gccggaggcc 960  
 cctcatgcct atggtcagat caggcttgcc ccagctgggc gtggaagggg ccaggccgg 1019

<210> 36  
 <211> 93  
 <212> DNA  
 <213> Canis familiaris

<400> 36  
 atgatagtgc tggcgccagc ctggagccca actgtgcgta taccggggg acaaggcggg 60  
 ggacaggcag agcgctaccg agctgggcag agc 93

<210> 37  
 <211> 93  
 <212> DNA  
 <213> Canis familiaris

<400> 37  
 gctctgccca gctcggtage gctctgctg tccccgcct tgtccccgg gtatacgcac 60  
 agttgggctc caggctggcg ccagcactat cat 93

<210> 38  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 38  
 tgaattcgga cataacttca atattac 27

<210> 39  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 Primer

<400> 39  
 tctcgagatt cagcttcaat gcctgta 27

<210> 40  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 40

cccaagctta tgggtctcac ctcccaac

28

<210> 41

<211> 395

<212> DNA

<213> Felis catus

<400> 41

ggccataggc atgaagggcc tccggccgag atgatagtgc tggcgccagc ctggagccca 60

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tccttcagcc acagccccat ctctccacc ttcaaggcca ccatccgaaa gctgtctgat 180

tacctgcttc aggattaccc agtcaccgtc gcctccaacc tacaggacga cgagctctgt 240

gggccattct ggcacctggt cctggcccag cgctggatgg gtcggctcaa ggctgtggct 300

gggtcccaga tgcaaagcct gctggaggcg gtcaacaccg agatacattt tgtcaccttg 360

tgtgccttcc agccccctcc cagctgtctt cgatt 395

<210> 42

<211> 793

<212> DNA

<213> Felis catus

<400> 42

cttcaaggta accatccgaa agctgtctga ttacctgctt caggattacc cagtcaccgt 60

cgctccaac ctacaggacg acgagctctg tgggccattc tggcacctgg tcctggccca 120

gcgctggatg ggtcggctca aggctgtggc tgggtcccag atgcaaagcc tgctggaggc 180

ggtcaacacc gagatacatt ttgtcacctt gtgtgccttc cagccccctc ccagctgtct 240

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<212> DNA  
<213> Felis catus

<220>  
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<222> (31)..(903)

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Ser Pro Thr Thr Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu  
10 15 20  
cgc ggg tcc ccc gac tgt tcc ttc agc cac agc ccc atc tcc tcc acc 150  
Arg Gly Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr  
25 30 35 40  
ttc aag gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac 198  
Phe Lys Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
45 50 55  
cca gtc acc gtc gcc tcc aac cta cag gac gac gag ctc tgt ggg cca 246  
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro  
60 65 70  
ttc tgg cac ctg gtc ctg gcc cag cgc tgg atg ggt cgg ctc aag gct 294

Phe Trp His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala  
75 80 85

gtg gct ggg tcc cag atg caa agc ctg ctg gag gcg gtc aac acc gag 342  
Val Ala Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu  
90 95 100

ata cat ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt 390  
Ile His Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu  
105 110 115 120

cga ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag 438  
Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu  
125 130 135

cag ctg gcg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcg ggg 486  
Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly  
140 145 150

tgc ctg gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc cca 534  
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro  
155 160 165

agg agc ccc agg gcc ttg gag gcc aca gcc ctg cca gcc cct cag gcc 582  
Arg Ser Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala  
170 175 180

cct ctg ctg ctc ctc ctg ctg ctg ttg cct gtg gct ctc ttg ctg atg 630  
Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met  
185 190 195 200

tcc gcc gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc 678  
Ser Ala Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro  
205 210 215

tac ccc agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac 726  
Tyr Pro Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His  
220 225 230

ctg ccc gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act 774  
Leu Pro Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr  
235 240 245

ggt tcc ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg 822  
Gly Ser Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp  
250 255 260

agg caa cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc 870



Arg Gln Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu  
265 270 275 280

tgt aca aag tcc ttg tcc tca gga aat tgt ata taaatcatcc ttttctacca 923  
Cys Thr Lys Ser Leu Ser Ser Gly Asn Cys Ile  
285 290

aaaaaaaaa aaaaaaaaaa 942

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<211> 291  
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<213> Felis catus

<400> 44  
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Ser His Ser Pro Ile Ser Ser Thr Phe Lys Val Thr Ile Arg Lys Leu  
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
50 55 60

Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp His Leu Val Leu Ala Gln  
65 70 75 80

Arg Trp Met Gly Arg Leu Lys Ala Val Ala Gly Ser Gln Met Gln Ser  
85 90 95

Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Leu Cys Ala  
100 105 110

Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
115 120 125

His Leu Leu Gln Asp Thr Ser Glu Gln Leu Ala Ala Leu Lys Pro Trp  
130 135 140

Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro  
145 150 155 160

Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser Pro Arg Ala Leu Glu Ala  
165 170 175

Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu Leu Leu Leu Leu Leu Leu  
 180 185 190

Leu Pro Val Ala Leu Leu Leu Met Ser Ala Ala Trp Cys Leu His Trp  
 195 200 205

Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro Arg Glu Gln Arg Lys Thr  
 210 215 220

Leu Arg Pro Arg Glu Arg Asn His Leu Pro Glu Asp Thr Glu Pro Gly  
 225 230 235 240

Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser Phe Leu Asp His Ala Ala  
 245 250 255

Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln Arg Gln Pro Pro Thr Pro  
 260 265 270

Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr Lys Ser Leu Ser Ser Gly  
 275 280 285

Asn Cys Ile  
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 <213> Felis catus

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 ccatcccgga gggagagtga gcggggcagc gtggctcagg aaggaaccag tctctagctg 180  
 actttctccg agtcccggtt ctgtgtcctc gggcagggtga ttctctctc tgggcctcag 240  
 tgtcttctc tgctccctgg ggtagggcgt tctccatctc cttcttcgcc agtgcaggca 300  
 ccaggcggcg gacatcagca agagagccac aggcaacagc agcaggagga gcagcagagg 360  
 ggcctgaggg gctggcaggg ctgtggcctc caaggccctg gggctccttg ggggcagtgg 420  
 ggtggaggag tcgggctgac actgtagctc caggcacccc gagaaattcc tgcggggtgat 480



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<210> 47  
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 <212> DNA  
 <213> Felis catus

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 gaaggaacca gtctctagct gactttctcc gagtcccggc tctgtgtcct cgggcaggtg 180  
 attcctctct ctgggcctca gtgtcttctc ctgctccctg gggtagggcg ttctccatct 240  
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 acacaaggtg acaaaatgta tctcgtgtgt gaccgcctcc agcaggcttt gcatctggga 600  
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 gtaatcagac agctttcggg tggtgacctt gaaggtggag gagatggggc tgtggctgaa 780  
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 agttgggctc caggctggcg ccagcactat cat 873

<210> 48  
 <211> 795  
 <212> DNA  
 <213> Felis catus

<220>

<221> CDS

<222> (1)..(795)

<400> 48

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1				5					10					15		

gtc	acc	atc	cga	aag	ctg	tct	gat	tac	ctg	ctt	cag	gat	tac	cca	gtc	96
Val	Thr	Ile	Arg	Lys	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	
			20					25					30			

acc	gtc	gcc	tcc	aac	cta	cag	gac	gac	gag	ctc	tgt	ggg	cca	ttc	tgg	144
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Asp	Glu	Leu	Cys	Gly	Pro	Phe	Trp	
			35				40					45				

cac	ctg	gtc	ctg	gcc	cag	cgc	tgg	atg	ggc	cgc	ctc	aag	gct	gtg	gct	192
His	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Gly	Arg	Leu	Lys	Ala	Val	Ala	
	50					55					60					

ggg	tcc	cag	atg	caa	agc	ctg	ctg	gag	gcg	gtc	aac	acc	gag	ata	cat	240
Gly	Ser	Gln	Met	Gln	Ser	Leu	Leu	Glu	Ala	Val	Asn	Thr	Glu	Ile	His	
65				70					75					80		

ttt	gtc	acc	ttg	tgt	gcc	ttc	cag	ccc	ctc	ccc	agc	tgt	ctt	cga	ttc	288
Phe	Val	Thr	Leu	Cys	Ala	Phe	Gln	Pro	Leu	Pro	Ser	Cys	Leu	Arg	Phe	
				85				90						95		

gtc	cag	acc	aac	atc	tcc	cac	ctc	ctg	cag	gac	acc	tcc	gag	cag	ctg	336
Val	Gln	Thr	Asn	Ile	Ser	His	Leu	Leu	Gln	Asp	Thr	Ser	Glu	Gln	Leu	
			100					105					110			

gcg	gcc	ttg	aag	ccc	tgg	atc	acc	cgc	agg	aat	ttc	tcg	ggg	tgc	ctg	384
Ala	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Arg	Asn	Phe	Ser	Gly	Cys	Leu	
		115					120					125				

gag	cta	cag	tgt	cag	ccc	gac	tcc	tcc	acc	cca	ctg	ccc	cca	agg	agc	432
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Pro	Leu	Pro	Pro	Arg	Ser	
	130					135					140					

ccc	agg	gcc	ttg	gag	gcc	aca	gcc	ctg	cca	gcc	cct	cag	gcc	cct	ctg	480
Pro	Arg	Ala	Leu	Glu	Ala	Thr	Ala	Leu	Pro	Ala	Pro	Gln	Ala	Pro	Leu	
145					150				155					160		

ctg	ctc	ctc	ctg	ctg	ctg	ttg	cct	gtg	gct	ctc	ttg	ctg	atg	tcc	gcc	528
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Val	Ala	Leu	Leu	Leu	Met	Ser	Ala	
				165					170					175		

gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc tac ccc 576  
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro  
180 185 190

agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac ctg ccc 624  
Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro  
195 200 205

gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act ggt tcc 672  
Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser  
210 215 220

ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg agg caa 720  
Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln  
225 230 235 240

cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc tgt aca 768  
Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr  
245 250 255

aag tcc ttg tcc tca gga aat tgt ata 795  
Lys Ser Leu Ser Ser Gly Asn Cys Ile  
260 265

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<211> 265  
<212> PRT  
<213> Felis catus

<400> 49  
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20 25 30

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35 40 45

His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala Val Ala  
50 55 60

Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu Ile His  
65 70 75 80

Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe

85

90

95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu Gln Leu  
100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu  
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser  
130 135 140

Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu  
145 150 155 160

Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Ala  
165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro  
180 185 190

Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro  
195 200 205

Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser  
210 215 220

Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln  
225 230 235 240

Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr  
245 250 255

Lys Ser Leu Ser Ser Gly Asn Cys Ile  
260 265

<210> 50

<211> 795

<212> DNA

<213> Felis catus

<400> 50

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gaaggaacca gtctctagct gactttctcc gagtcccggc tctgtgtcct cgggcaggtg 180





<221> CDS

<222> (196)..(1017)

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tgcccaacga agccggccac gattgggtccc cgaagacccc gcccatctcc tgggcggggc 120

gggcgggggc aagggtctggg gagttactaa agacatcccc gcgcccctac tccgctgcct 180

gctattcacc tcgcc atg gtt ctc ctg cct ctg cgc tgt ctc ttc tgg ggc 231

Met Val Leu Leu Pro Leu Arg Cys Leu Phe Trp Gly

1

5

10

tcc ttg ttg acc acc gtc tac cca gaa cca cgc act gca tgc aga gaa 279

Ser Leu Leu Thr Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu

15

20

25

aag caa tac cta gta gac agt cag tgc tgt aat atg tgc cca cca gga 327

Lys Gln Tyr Leu Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly

30

35

40

gag aaa ctg gtg aat gac tgc cta cat acc att gac acg gaa tgc act 375

Glu Lys Leu Val Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr

45

50

55

60

cgt tgc caa aca ggc gaa ttc cta gac act tgg aac gca gag aga cac 423

Arg Cys Gln Thr Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His

65

70

75

tgt cac cag cac aaa tac tgc gac ccc aac cta ggg ctc cat gtc gag 471

Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu

80

85

90

aag gag ggc acg tca gaa aca gac acc act tgc aca tgc gat gaa ggt 519

Lys Glu Gly Thr Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly

95

100

105

ctg cat tgt acc aac gct gcc tgt gag agc tgc acc atg cac agc ctg 567

Leu His Cys Thr Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu

110

115

120

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Cys Pro Pro Gly Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp

125

130

135

140

acc atc tgc gat ccc tgc ccc atc ggc ttc ttc tcc aat gtg tct tct 663

Thr Ile Cys Asp Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser

155

aaaaaaaaaa aaaaaaaa 1425

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 <213> Canis familiaris

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                     20                    25                    30  
 Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val  
                     35                    40                    45  
 Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr  
                     50                    55                    60  
 Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His  
     65                    70                    75                    80  
 Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr  
                     85                    90                    95  
 Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr  
                     100                    105                    110  
 Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly  
                     115                    120                    125  
 Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp  
     130                    135                    140  
 Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys  
     145                    150                    155                    160  
 Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln  
                     165                    170                    175  
 Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu  
                     180                    185                    190  
 Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val  
                     195                    200                    205  
 Leu Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn  
     210                    215                    220

Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met  
 225 230 235 240

Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln  
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Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu  
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Arg Val

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 <213> Canis familiaris

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<211> 822  
<212> DNA  
<213> Canis familiaris

<400> 55  
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tgcccaccag gagagaaact ggtgaatgac tgccacata ccattgacac ggaatgcact 180  
cgttgccaaa caggcgaatt cctagacact tggaacgcag agagacactg tcaccagcac 240  
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accacttgca catgcgatga aggtctgcat tgtaccaacg ctgcctgtga gagctgcacc 360  
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tgtcaccctt ggacaagctg tgaaacaaaa ggcctgggtga aggttcaggc gggaactaac 540  
aagactgatg ttatctgtgg tcccagcct cggttaagag ccctagtggg ggtccccatc 600  
attatgggga tcctgcttgt tgcctgttg gtgtctgcct gcatccgaaa ggtgggtcaag 660

aagccagaga ataaggttat gtatcaggac cctgtggagg acttggagga atttcctatg 720  
 cccccgcact ccattgctcc ggtgcaagag accttacatg ggtgccagcc cgtcacccag 780  
 gaggacggca aagagagccg catctccgtg caggagagag tg 822

<210> 56  
 <211> 822  
 <212> DNA  
 <213> Canis familiaris

<400> 56  
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 cccatgtaag gtctcttgca ccggagcaat ggagtgcggg ggcataggaa attcctccaa 120  
 gtctccaca gggctctgat acataacctt attctctggc ttcttgacca cctttcggat 180  
 gcaggcagac accaacagga caacaagcag gatccccata atgatgggga ccaccactag 240  
 ggctcttaac cgaggctggg gaccacagat aacatcagtc ttgttagttc ccgcctgaac 300  
 cttcaccagg cctttggttt cacagcttgt ccaagggtga cacttttcca aagcagaaga 360  
 cacattggag aagaagccga tggggcaggg atcgcagatg gtatcagaaa tccctgtagc 420  
 gatctgtttg actcccaggc caggggggca caggctgtgc atgggtgcagc tctcacaggc 480  
 agcgttggtg caatgcagac cttcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540  
 ctctttctcg acatggagcc ctaggttggg gtcgcagtat ttgtgctggt gacagtgtct 600  
 ctctgcgttc caagtgtcta ggaattcgcc tgtttggtgcaa cgagtgcatt ccgtgtcaat 660  
 ggtatgtagg cagtcattca ccagtttctc tccctgggtggg cacatattac agcactgact 720  
 gtctactagg tattgctttt ctctgcatgc agtgcgtggt tctgggtaga cgggtggtcaa 780  
 caaggagccc cagaagagac agcgcagagg caggagaacc at 822

<210> 57  
 <211> 765  
 <212> DNA  
 <213> Canis familiaris

<220>

<221> CDS

<222> (1)..(765)

<400> 57

cca gaa cca cgc act gca tgc aga gaa aag caa tac cta gta gac agt 48

Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu Val Asp Ser

1

5

10

15

cag tgc tgt aat atg tgc cca cca gga gag aaa ctg gtg aat gac tgc 96

Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys

20

25

30

cta cat acc att gac acg gaa tgc act cgt tgc caa aca ggc gaa ttc 144

Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe

35

40

45

cta gac act tgg aac gca gag aga cac tgt cac cag cac aaa tac tgc 192

Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys

50

55

60

gac ccc aac cta ggg ctc cat gtc gag aag gag ggc acg tca gaa aca 240

Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr

65

70

75

80

gac acc act tgc aca tgc gat gaa ggt ctg cat tgt acc aac gct gcc 288

Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr Asn Ala Ala

85

90

95

tgt gag agc tgc acc atg cac agc ctg tgc ccc cct ggc ctg gga gtc 336

Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val

100

105

110

aaa cag atc gct aca ggg att tct gat acc atc tgc gat ccc tgc ccc 384

Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro

115

120

125

atc ggc ttc ttc tcc aat gtg tct tct gct ttg gaa aag tgt cac cct 432

Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro

130

135

140

tgg aca agc tgt gaa acc aaa ggc ctg gtg aag gtt cag gcg gga act 480

Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr

145

150

155

160

aac aag act gat gtt atc tgt ggt ccc cag cct cgg tta aga gcc cta 528

Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu

165

170

175

gtg gtg gtc ccc atc att atg ggg atc ctg ctt gtt gtc ctg ttg gtg 576  
 Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val  
 180 185 190

tct gcc tgc atc cga aag gtg gtc aag aag cca gag aat aag gtt atg 624  
 Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met  
 195 200 205

tat cag gac cct gtg gag gac ttg gag gaa ttt cct atg ccc ccg cac 672  
 Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His  
 210 215 220

tcc att gct ccg gtg caa gag acc tta cat ggg tgc cag ccc gtc acc 720  
 Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr  
 225 230 235 240

cag gag gac ggc aaa gag agc cgc atc tcc gtg cag gag aga gtg 765  
 Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val  
 245 250 255

<210> 58  
 <211> 255  
 <212> PRT  
 <213> Canis familiaris

<400> 58  
 Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu Val Asp Ser  
 1 5 10 15

Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys  
 20 25 30

Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe  
 35 40 45

Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys  
 50 55 60

Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr  
 65 70 75 80

Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr Asn Ala Ala  
 85 90 95

Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val  
 100 105 110



Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro  
 115 120 125

Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro  
 130 135 140

Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr  
 145 150 155 160

Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu  
 165 170 175

Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val  
 180 185 190

Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met  
 195 200 205

Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His  
 210 215 220

Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr  
 225 230 235 240

Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val  
 245 250 255

<210> 59  
 <211> 765  
 <212> DNA  
 <213> Canis familiaris

<400> 59  
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 cccatgtaag gtctcttgca ccggagcaat ggagtgcggg ggcataggaa attcctccaa 120  
 gtctccaca gggctctgat acataacctt attctctggc ttcttgacca cctttcggat 180  
 gcaggcagac accaacagga caacaagcag gatccccata atgatgggga ccaccactag 240  
 ggctcttaac cgaggctggg gaccacagat aacatcagtc ttgttagttc ccgcctgaac 300  
 cttcaccagg cctttgggtt cacagcttgt ccaagggtga cacttttcca aagcagaaga 360  
 cacattggag aagaagccga tggggcaggg atcgcagatg gtatcagaaa tccctgtagc 420

gatctgtttg actcccaggc caggggggca caggctgtgc atgggtgcagc tctcacaggc 480  
 agcgttggtg caatgcagac cttcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540  
 ctctttctcg acatggagcc ctaggttggg gtcgcagtat ttgtgctggt gacagtgtct 600  
 ctctgcgttc caagtgtcta ggaattcgcc tgtttggcaa cgagtgcatt ccgtgtcaat 660  
 ggtatgtagg cagtcattca ccagtttctc tcttggtggg cacatattac agcactgact 720  
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<210> 60  
 <211> 336  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(336)

<400> 60  
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 Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu  
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 acc aaa ggc ctg gtg gag ctt cag gcg ggg acc aac aag acg gat gcc 96  
 Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala  
 20 25 30  
 gtc tgc ggt ttc cag gat cgg ata aga gcc ctg gtg gtg atc ccc atc 144  
 Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile  
 35 40 45  
 acg atg gtg gtc ctg ctt gct gtc ttg ttg gtg tct gcg tat atc aga 192  
 Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg  
 50 55 60  
 aag gtg acc aag aag cca gag aat aag gtc ctc cag cct aag gct gtg 240  
 Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val  
 65 70 75 80  
 tcg cag gac cct gtg gag gac ttg gag gtc ctt cct gtc ccc ctc cac 288  
 Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His  
 85 90 95

ccc att gct ccg gtg cag gag acc tta cac ggg tgc cag ccg gtc acc 336  
 Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr  
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<210> 61  
 <211> 112  
 <212> PRT  
 <213> Felis catus

<400> 61  
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Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala  
                   20                  25                  30

Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile  
                   35                  40                  45

Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg  
                   50                  55                  60

Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val  
                   65                  70                  75                  80

Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His  
                   85                  90                  95

Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr  
                   100                  105                  110

<210> 62  
 <211> 336  
 <212> DNA  
 <213> Felis catus

<400> 62  
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 aggaaggacc tccaagtcct ccacagggtc ctgcgacaca gccttaggct ggaggacctt 120  
 attctctggc ttcttgggtca cctttctgat atacgcagac accaacaaga cagcaagcag 180  
 gaccaccatc gtgatgggga tcaccaccag ggctcttata cgatcctgga aaccgcagac 240  
 ggcacccgtc ttgttgggtcc ccgcctgaag ctccaccagg cctttgggtct cacacctcgt 300

ccaaggtga cacttttccg aagcagatga cacatt

336

<210> 63

<211> 390

<212> DNA

<213> Canis familiaris

<400> 63

ataagtgagg ctagtagtaa cccagcgtcc gttctgcggt gggcgccaaa aggtactac 60  
accataagca gcaacctggt gagcctcgag aatgggaaac agttggccgt gaaaagacaa 120  
ggactctatt acgtctatgc ccaagtcacc ttctgctcca atcgggcagc ttcgagtcaa 180  
gctccgttcg tcgccagcct atgcctccat tccccgagtg gaacggagag agtcttactc 240  
cgcgccgga gctcccgcg ctcgtccaaa ccttgcggcc aacagtccat ccacttggga 300  
ggagtatttg aattgcatcc aggtgcttcg gtgttcgtca acgtgactga tccaagccaa 360  
gtgagccacg ggaccggctt cacgtctttt 390

<210> 64

<211> 1878

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (284)..(1063)

<400> 64

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tttgctggga gagaagacta cgaagcacat tttccaggaa gtgtgggctg caacgattgt 180  
gcgctcttaa ctaatcctga gtaagggtggc cactttgaca gtgttttcat gctgcctctg 240  
ccaccttctc ggtctgaaga tatcatttca actctaacac agc atg atc gaa aca 295  
Met Ile Glu Thr  
1  
tat agc caa act gct ccc cga tct gtg gcc act gga cca ccc gtc agt 343

222

Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Thr Gly Pro Pro Val Ser  
 5 10 15 20

atg aaa att ttt atg tat ttg ctt act gtt ttt ctc atc acc cag atg 391  
 Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln Met  
 25 30 35

att gga tcg gca ctc ttt gct gta tat ctt cac aga aga ttg gac aag 439  
 Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp Lys  
 40 45 50

ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc atg aaa acg 487  
 Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe Met Lys Thr  
 55 60 65

tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta ctg aac tgt 535  
 Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys  
 70 75 80

gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag ata atg cta 583  
 Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu Ile Met Leu  
 85 90 95 100

aac aac gaa atg aag aaa gaa gaa aac att gca atg caa aaa ggt gat 631  
 Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln Lys Gly Asp  
 105 110 115

cag gat cct cga att gca gcc cat gtc ata agt gag gct agt agt aac 679  
 Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Asn  
 120 125 130

cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac acc ata agc 727  
 Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr Thr Ile Ser  
 135 140 145

agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc gtg aaa aga 775  
 Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg  
 150 155 160

caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc tcc aat cgg 823  
 Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg  
 165 170 175 180

gca gct tcg agt caa gct ccg ttc gtc gcc agc cta tgc ctc cat tcc 871  
 Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys Leu His Ser  
 185 190 195

ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc tcc cgc ggc 919

223

Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser Ser Arg Gly  
 200 205 210

tcg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga gga gta ttt 967  
 Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe  
 215 220 225

gaa ttg cat cca ggt gct tgc gtg ttc gtc aac gtg act gat cca agc 1015  
 Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser  
 230 235 240

caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta ctc aaa ctc 1063  
 Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu  
 245 250 255 260

tgagtgtctg cacctcacag gctgcagctc agctcctgtt ggtggtcttc gtaatacggc 1123

cgagcagtta agaccaccac cctgttgaa ctgcctatct ataaccctag gatcctcctc 1183

gtggagaact atttattata caccoccagg cgtggagggc tgcaagaagg gaatgacagg 1243

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cactgatgca gacatccaga gagtcccatg aaaaagacga gactattatg cacagattga 1363

atcctcagta aacggcagat aattagtcca gtttcgtttt gtttctttgc atgcagtgtc 1423

tttactgga gaatgtactc gatttccccg cgaagatgct gaagggcaac agggagcctc 1483

agctcacagt cagttacggt tgaccggggg tccccggggc cccgatggag gggacaggct 1543

ccagaaagtc tgatggcgcg gagaactgga aaaccctgcc cccaccagcc accctgacac 1603

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ttatttcaac cctgttgct ctccaccagt gtaggcggga ggagagagca gaggctgccc 1723

actcctctc ctgaaatgac tgtattttaa ggaaatctct cctacctacc tgcagtctcc 1783

attgtttcca gagtgaactt gtgattatct tggtatttat tttttgaata ataaagcgcc 1843

cttaacgtta aaaaaaaaaa aaaaaaaaaa aaaaa 1878

<210> 65

<211> 260

<212> PRT

<213> Canis familiaris

<400> 65

Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Thr Gly  
1 5 10 15

Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg  
35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val  
50 55 60

Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser  
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys  
85 90 95

Glu Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met  
100 105 110

Gln Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu  
115 120 125

Ala Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr  
130 135 140

Tyr Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu  
145 150 155 160

Ala Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe  
165 170 175

Cys Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu  
180 185 190

Cys Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala  
195 200 205

Ser Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu  
210 215 220

Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val  
225 230 235 240

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly

225

Leu Leu Lys Leu  
260

<210> 66  
<211> 1878  
<212> DNA  
<213> *Canis familiaris*

<400> 66  
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 tttcctttta atacagtcatt ttcaggagga ggagtgggca gcctctgctc tctcctcccg 180  
 cctacactgg tggagaggca acaggggtga aataagataa ccgattagca acagcctgac 240  
 tgtgggggga ggggggcgga ggaggagag aatgagtgtc agggtggtctg gtgggggcag 300  
 ggttttccag ttctccgcgc catcagactt tctggagcct gtcccctcca tcggggcccc 360  
 ggggaccccg ggtcaaccgt aactgactgt gagctgaggc tccctgttgc ccttcagcat 420  
 ctctcggggg aaatcgagta cattctccag tgaaagacac tgcattgcaa gaaacaaaac 480  
 gaaactggac taattatctg ccgtttactg aggattcaat ctgtgcataa tagtctcgtc 540  
 tttttcatgg gactctctgg atgtctgcat cagtggggcg gctgcttcca gaatatcaac 600  
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 ggcagttcaa caggggtggt ggtcttaact gctcggccgt attacgaaga ccaccaacag 780  
 gagctgagct gcagcctgtg aggtgccagc actcagagtt tgagtaagcc aaaagacgtg 840  
 aagccgggtcc cgtggctcac ttggcttggga tcagtcacgt tgacgaacac cgaagcacct 900  
 ggatgcaatt caaatactcc tcccaagtgg atggactgtt ggccgcaagg tttggacgag 960  
 ccgcgggagc tcgcggcgcg gagtaagact ctctccgttc cactcgggga atggaggcat 1020  
 aggctggcga cgaacggagc ttgactcgaa gctgcccgat tggagcagaa ggtgacttgg 1080



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 ttactactag cctcacttat gacatgggct gcaattcgag gatcctgac acctttttgc 1260  
 attgcaatgt tttcttcttt cttcatttcg ttgttttagca ttatctcctt gagaaaggct 1320  
 tcaaattggc ttttaatttc ctcacagttc agtaaggaca aggacccctc ccctttgttg 1380  
 cttttctgta acgttttcat gaacacaaaa tcttcataaa gattcctttc atcttctatc 1440  
 ttgtccaatc ttctgtgaag atatacagca aagagtgccg atccaatcat ctgggtgatg 1500  
 agaaaaacag taagcaaata cataaaaatt ttcatactga cgggtgggtcc agtggccaca 1560  
 gatcgggggag cagtttgggt atatgtttcg atcatgctgt gttagagttg aaatgatatc 1620  
 ttcagaccga gaaggtggca gaggcagcat gaaaacactg tcaaagtggc caccttactc 1680  
 aggattagtt aagagcgcac aatcgttgca gccacactt cctggaaaat gtgcttcgta 1740  
 gtcttctctc ccagcaaaaa aagttacgta aaggtttttt tttttttttt tttttttttt 1800  
 taattatacc catatcattc acttccaggc tttccctttt gttagtaaag aagaaacaag 1860  
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<210> 67  
 <211> 780  
 <212> DNA  
 <213> Canis familiaris

<400> 67  
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 ctctttgctg tatatcttca cagaagattg gacaagatag aagatgaaag gaatctttat 180  
 gaagattttg tgttcatgaa aacgttacag aaatgcaaca aaggggaggg gtccttgtcc 240  
 ttactgaact gtgaggaaat taaaagccaa tttgaagcct ttctcaagga gataatgcta 300  
 aacaacgaaa tgaagaaaga agaaaacatt gcaatgcaaa aaggtgatca ggatcctcga 360  
 attgcagccc atgtcataag tgaggctagt agtaaccag cgtccgttct gcgggtggcg 420

ccaaaagggt actacaccat aagcagcaac ctggtgagcc tcgagaatgg gaaacagttg 480  
gccgtgaaaa gacaaggact ctattacgtc tatgcccaag tcaccttctg ctccaatcgg 540  
gcagcttcga gtcaagctcc gttcgtcgcc agcctatgcc tccattcccc gagtggaaacg 600  
gagagagtct tactccgcgc cgcgagctcc cgcggctcgt ccaaaccttg cggccaacag 660  
tccatccact tgggaggagt atttgaattg catccagggtg cttcgggtgtt cgtcaacgtg 720  
actgatccaa gccaaagtga ccacgggacc ggcttcacgt cttttggctt actcaaactc 780

<210> 68

<211> 780

<212> DNA

<213> Canis familiaris

<400> 68

gagtttgagt aagccaaaag acgtgaagcc ggtcccgtag ctcacttggc ttggatcagt 60  
cacgttgacg aacaccgaag cacctggatg caattcaaat actcctccca agtggatgga 120  
ctgttggccg caaggtttgg acgagccgcg ggagctcgcg gcgcggagta agactctctc 180  
cgttccactc ggggaatgga ggcataggct ggcgacgaac ggagcttgac tcgaagctgc 240  
ccgattggag cagaaggtga cttgggcata gacgtaatag agtccttgtc ttttcacggc 300  
caactgtttc ccattctcga ggctcaccag gttgctgctt atgggtgtagt acccttttgg 360  
cgcccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420  
tcgaggatcc tgatcacctt tttgcattgc aatgttttct tctttcttca tttcgttggt 480  
tagcattatc tccttgagaa aggcttcaaa ttggctttta atttcctcac agttcagtaa 540  
ggacaaggac cctccccctt tgttgcatth ctgtaacgtt ttcattgaaca caaaatcttc 600  
ataaagattc ctttcatctt ctatcttgtc caatcttctg tgaagatata cagcaaagag 660  
tgccgatcca atcatctggg tgatgagaaa aacagtaagc aaatacataa aaattttcat 720  
actgacgggt ggtccagtgg ccacagatcg gggagcagtt tggctatatg tttcgatcat 780

<210> 69

<211> 633  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(633)

<400> 69

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Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe	
1 5 10 15	
atg aaa acg tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta	96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu	
20 25 30	
ctg aac tgt gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag	144
Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu	
35 40 45	
ata atg cta aac aac gaa atg aag aaa gaa gaa aac att gca atg caa	192
Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln	
50 55 60	
aaa ggt gat cag gat cct cga att gca gcc cat gtc ata agt gag gct	240
Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala	
65 70 75 80	
agt agt aac cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac	288
Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr	
85 90 95	
acc ata agc agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc	336
Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala	
100 105 110	
gtg aaa aga caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc	384
Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys	
115 120 125	
tcc aat cgg gca gct tcg agt caa gct ccg ttc gtc gcc agc cta tgc	432
Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys	
130 135 140	
ctc cat tcc ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc	480
Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser	
145 150 155 160	

229

tcc cgc ggc tcg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga 528  
 Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly  
 165 170 175

gga gta ttt gaa ttg cat cca ggt gct tcg gtg ttc gtc aac gtg act 576  
 Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr  
 180 185 190

gat cca agc caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta 624  
 Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu  
 195 200 205

ctc aaa ctc 633  
 Leu Lys Leu  
 210

<210> 70  
 <211> 211  
 <212> PRT  
 <213> Canis familiaris

<400> 70  
 Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe  
 1 5 10 15

Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu  
 20 25 30

Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu  
 35 40 45

Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln  
 50 55 60

Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala  
 65 70 75 80

Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr  
 85 90 95

Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala  
 100 105 110

Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys  
 115 120 125

230

Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys  
 130 135 140

Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser  
 145 150 155 160

Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly  
 165 170 175

Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr  
 180 185 190

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu  
 195 200 205

Leu Lys Leu  
 210

<210> 71  
 <211> 633  
 <212> DNA  
 <213> Canis familiaris

<400> 71  
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 ctgttggccg caaggtttgg acgagccgcg ggagctcgcg gcgcggagta agactctctc 180  
 cgttccactc ggggaatgga ggcataaggct ggcgacgaac ggagcttgac tcgaagctgc 240  
 ccgattggag cagaagggtga cttgggcata gacgtaatat agtccttgtc ttttcacggc 300  
 caactgtttc ccattctoga ggctcaccag gttgctgctt atggtgtagt acccttttgg 360  
 cgcccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420  
 tcgaggatcc tgatcacctt tttgcattgc aatgttttct tctttcttca tttcgttggt 480  
 tagcattatc tccttgagaa aggcttcaaa ttggctttta atttcctcac agttcagtaa 540  
 ggacaaggac cctcccccct tgttgcatct ctgtaacggt ttcattgaaca caaaatcttc 600  
 ataaagattc ctttcatctt ctatcttgct caa 633

<210> 72  
 <211> 885  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (29)..(808)

<400> 72

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gaagatacca tttcaacttt aacacagc atg atc gaa aca tat agc caa act      52
                        Met Ile Glu Thr Tyr Ser Gln Thr
                          1                      5

gct ccc cgc tcc gtg gcc cct gga cca ccc gtc agt atg aaa att ttt      100
Ala Pro Arg Ser Val Ala Pro Gly Pro Pro Val Ser Met Lys Ile Phe
      10                      15                      20

atg tat tta ctt act gtg ttt ctc atc acc cag atg att ggg tca gca      148
Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln Met Ile Gly Ser Ala
      25                      30                      35                      40

ctc ttt gct gtg tat ctt cac aga aga ctg gac aag ata gaa gat gaa      196
Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp Lys Ile Glu Asp Glu
                        45                      50                      55

agg aat ctt tat gaa gat ttt gtg ttc atg aaa aca tta cag aaa tgc      244
Arg Asn Leu Tyr Glu Asp Phe Val Phe Met Lys Thr Leu Gln Lys Cys
                        60                      65                      70

aac aaa gga gag ggg gcc tta tcc tta ctg aac tgt gag gaa att aaa      292
Asn Lys Gly Glu Gly Ala Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys
                        75                      80                      85

agc cgg ttt gaa gcc ttt ctc aag gag ata atg cta aac aaa gaa acg      340
Ser Arg Phe Glu Ala Phe Leu Lys Glu Ile Met Leu Asn Lys Glu Thr
                        90                      95                      100

aag aaa gaa aaa aat gtt gca atg caa aaa ggc gac cag gat cct cga      388
Lys Lys Glu Lys Asn Val Ala Met Gln Lys Gly Asp Gln Asp Pro Arg
      105                      110                      115                      120

gtt gca gca cat gtc ata agt gag gcc agc agt agc aca gcg tct gtt      436
Val Ala Ala His Val Ile Ser Glu Ala Ser Ser Ser Thr Ala Ser Val
                        125                      130                      135

ctc cag tgg gcc ccc aaa ggc tac tac acc ata agc agc aac ttg gtg      484
Leu Gln Trp Ala Pro Lys Gly Tyr Tyr Thr Ile Ser Ser Asn Leu Val

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232

140

145

150

acc ctc gag aac ggg aag cag ctg gcc gtt aaa aga caa gga ctc tat 532  
 Thr Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg Gln Gly Leu Tyr  
 155 160 165

tat atc tac gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt 580  
 Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser  
 170 175 180

caa gct ccg ttc ata gcc agc ctc tgc ctg cat tcc ccg agt gga tcc 628  
 Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu His Ser Pro Ser Gly Ser  
 185 190 195 200

gag aga gtc tta ctc aga gct gca aat gcc cgc agt tcc tcc aaa ccc 676  
 Glu Arg Val Leu Leu Arg Ala Ala Asn Ala Arg Ser Ser Ser Lys Pro  
 205 210 215

tgt ggg cag caa tcc att cac ttg gga gga gtc ttc gaa ctg cat cca 724  
 Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu His Pro  
 220 225 230

ggg gct tcg gtg ttc gtg aac gtg act gat ccg agc caa gtg agc cac 772  
 Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His  
 235 240 245

ggg acg ggc ttc acg tct ttt ggc ttg ctc aaa ctc tgaacactgg 818  
 Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu  
 250 255 260

cacctcgag gccgcgagggc ctgcaggccg cggctgagct cacgctggga gtcttcacaa 878

tacagca 885

<210> 73  
 <211> 260  
 <212> PRT  
 <213> Felis catus

<400> 73  
 Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Pro Gly  
 1 5 10 15

Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
 20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg

35

40

45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val  
50 55 60

Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser  
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys  
85 90 95

Glu Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met  
100 105 110

Gln Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu  
115 120 125

Ala Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr  
130 135 140

Tyr Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu  
145 150 155 160

Ala Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe  
165 170 175

Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu  
180 185 190

Cys Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala  
195 200 205

Asn Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu  
210 215 220

Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val  
225 230 235 240

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly  
245 250 255

Leu Leu Lys Leu  
260

<210> 74  
<211> 885  
<212> DNA



<213> Felis catus

<400> 74

tgctgtatta tgaagactcc cagcgtgagc tcagccgcgg cctgcaggcc tcgcggcctg 60  
cgagggtgcca gtgttcagag tttgagcaag ccaaaagacg tgaagcccgt cccgtggctc 120  
acttggctcg gatcagtcac gttcacgaac accgaagcac ctggatgcag ttcgaagact 180  
cctcccaagt gaatggattg ctgcccacag ggtttggagg aactgcgggc atttgcagct 240  
ctgagtaaga ctctctcgga tccactcggg gaatgcaggc agaggctggc tatgaacgga 300  
gcttgactcg aagcttcccg attggaacag aagggtgactt gggcgtagat ataatagagt 360  
ccttgtcttt taacggccag ctgcttcccg ttctcgaggg tcaccaagtt gctgcttatg 420  
gtgtagtagc ctttgggggc cactggaga acagacgctg tgctactgct ggcctcactt 480  
atgacatgtg ctgcaactcg aggatcctgg tcgccttttt gcattgcaac atttttttct 540  
ttcttcgttt ctttgttttag cattatctcc ttgagaaagg cttcaaaccg gcttttaatt 600  
tcctcacagt tcagtaagga taaggccccc tctcctttgt tgcatttctg taatgttttc 660  
atgaacacaa aatcttcata aagattcctt tcactttcta tcttgtccag tcttctgtga 720  
agatacacag caaagagtgc tgacccaatc atctgggtga tgagaaacac agtaagtaaa 780  
tacataaaaa ttttcatact gacgggtggt ccaggggcca cggagcgggg agcagtttgg 840  
ctatatgttt cgatcatgct gtgttaaagt tgaaatggta tcttc 885

<210> 75

<211> 780

<212> DNA

<213> Felis catus

<400> 75

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atgaaaattt ttatgtattt acttactgtg tttctcatca cccagatgat tgggtcagca 120  
ctctttgctg tgtatcttca cagaagactg gacaagatag aagatgaaag gaatctttat 180  
gaagattttg tgttcatgaa aacattacag aaatgcaaca aaggagaggg ggccttatcc 240

235

ttactgaact gtgaggaaat taaaagccgg tttgaagcct ttctcaagga gataatgcta 300  
 aacaaagaaa cgaagaaaga aaaaaatggt gcaatgcaaa aaggcgacca ggatcctcga 360  
 gttgcagcac atgtcataag tgaggccagc agtagcacag cgtctgttct ccagtgggcc 420  
 cccaaaggct actacaccat aagcagcaac ttggtgaccc tcgagaacgg gaagcagctg 480  
 gccgttaaaa gacaaggact ctattatatac tacgccaag tcaccttctg ttccaatcgg 540  
 gaagcttcga gtcaagctcc gttcatagcc agcctctgcc tgcattcccc gagtggatcc 600  
 gagagagtct tactcagagc tgcaaatgcc cgcagttcct ccaaaccctg tgggcagcaa 660  
 tccattcact tgggaggagt cttcgaactg catccagggtg cttcgggtgtt cgtgaacgtg 720  
 actgatccga gccaaagtga ccaaggagc ggcttcacgt cttttggctt gctcaaactc 780

<210> 76  
 <211> 780  
 <212> DNA  
 <213> Felis catus

<400> 76  
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 ttgctgcca cagggtttgg aggaactgag ggcatttgca gctctgagta agactctctc 180  
 ggatccactc ggggaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240  
 ccgattggaa cagaagggtga cttgggcgta gatataatag agtccttgtc ttttaacggc 300  
 cagctgcttc ccgttctcga gggtcaccaa gttgctgctt atggtgtagt agcctttggg 360  
 ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420  
 tcgaggatcc tggtcgcctt ttgcatlgc aacatttttt tctttcttcg tttctttgtt 480  
 tagcattatc tccttgagaa aggcttcaaa ccggctttta atttctcac agttcagtaa 540  
 ggataaggcc ccctctcctt tgttgcatth ctgtaatgtt ttcattgaaca caaaatcttc 600  
 ataaagattc ctttcatctt ctatcttgtc cagtcttctg tgaagataca cagcaaagag 660  
 tgctgacca atcatctggg tgatgagaaa cacagtaagt aaatacataa aaattttcat 720

actgacgggt ggtccagggg ccacggagcg gggagcagtt tggctatatg tttcgatcat 780

<210> 77  
<211> 633  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (1)..(633)

<400> 77

ctg gac aag ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc 48  
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe  
1 5 10 15

atg aaa aca tta cag aaa tgc aac aaa gga gag ggg gcc tta tcc tta 96  
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu  
20 25 30

ctg aac tgt gag gaa att aaa agc cgg ttt gaa gcc ttt ctc aag gag 144  
Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu  
35 40 45

ata atg cta aac aaa gaa acg aag aaa gaa aaa aat gtt gca atg caa 192  
Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln  
50 55 60

aaa ggc gac cag gat cct cga gtt gca gca cat gtc ata agt gag gcc 240  
Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala  
65 70 75 80

agc agt agc aca gcg tct gtt ctc cag tgg gcc ccc aaa ggc tac tac 288  
Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr  
85 90 95

acc ata agc agc aac ttg gtg acc ctc gag aac ggg aag cag ctg gcc 336  
Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala  
100 105 110

gtt aaa aga caa gga ctc tat tat atc tac gcc caa gtc acc ttc tgt 384  
Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys  
115 120 125

tcc aat cgg gaa gct tcg agt caa gct ccg ttc ata gcc agc ctc tgc 432  
Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys

130

135

140

ctg cat tcc ccg agt gga tcc gag aga gtc tta ctc aga gct gca aat 480  
 Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn  
 145 150 155 160

gcc cgc agt tcc tcc aaa ccc tgt ggg cag caa tcc att cac ttg gga 528  
 Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly  
 165 170 175

gga gtc ttc gaa ctg cat cca ggt gct tcg gtg ttc gtg aac gtg act 576  
 Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr  
 180 185 190

gat ccg agc caa gtg agc cac ggg acg ggc ttc acg tct ttt ggc ttg 624  
 Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu  
 195 200 205

ctc aaa ctc 633  
 Leu Lys Leu  
 210

<210> 78  
 <211> 211  
 <212> PRT  
 <213> Felis catus

<400> 78  
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 1 5 10 15

Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu  
 20 25 30

Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu  
 35 40 45

Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln  
 50 55 60

Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala  
 65 70 75 80

Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr  
 85 90 95

Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala

100

105

110

Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys  
 115 120 125

Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys  
 130 135 140

Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn  
 145 150 155 160

Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly  
 165 170 175

Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr  
 180 185 190

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu  
 195 200 205

Leu Lys Leu  
 210

<210> 79  
 <211> 633  
 <212> DNA  
 <213> Felis catus

<400> 79  
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 ttgctgcca cagggtttgg aggaactgcg ggcatttgca gctctgagta agactctctc 180  
 ggatccactc ggggaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240  
 ccgattggaa cagaaggtga cttgggcgta gatataatag agtccttgctc ttttaacggc 300  
 cagctgcttc ccgttctcga gggtcaccaa gttgctgctt atgggtgtagt agcctttggg 360  
 ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420  
 tcgaggatcc tggtcgcctt ttgcatgac aacatttttt tctttcttcg tttctttgtt 480  
 tagcattatc tccttgagaa aggccttcaaa ccggcctttta atttcctcac agttcagtaa 540

ggataaggcc ccctctcctt tgttgcattt ctgtaatggt ttcatagaaca caaaatcttc 600

ataaagattc ctttcatctt ctatcttgtc cag 633

<210> 80

<211> 610

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (29)..(430)

<400> 80

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1 5

ttg cta gct ctt ggg gct gcc tat gtt tct gcc ttt gct gta gaa aat 100  
Leu Leu Ala Leu Gly Ala Ala Tyr Val Ser Ala Phe Ala Val Glu Asn  
10 15 20

ccc atg aat aga ctg gtg gca gag acc ttg aca ctg ctc tcc act cat 148  
Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr Leu Leu Ser Thr His  
25 30 35 40

cga act tgg ctg ata ggc gat ggg aac ctg atg att cct act cct gaa 196  
Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro Glu  
45 50 55

aat aaa aat cac caa ctg tgc att aaa gaa gtt ttt cag ggt ata gac 244  
Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val Phe Gln Gly Ile Asp  
60 65 70

aca ttg aag aac caa act gcc cac ggg gag gct gtg gat aaa cta ttc 292  
Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala Val Asp Lys Leu Phe  
75 80 85

caa aac ttg tct tta ata aaa gaa cac ata gag cgc caa aaa aaa agg 340  
Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu Arg Gln Lys Lys Arg  
90 95 100

tgt gca gga gaa aga tgg aga gtg aca aag ttc cta gac tac ctg caa 388  
Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe Leu Asp Tyr Leu Gln  
105 110 115 120

gta ttt ctt ggt gta ata aac acc gag tgg aca ccg gaa agt 430

Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Pro Glu Ser  
125 130

tgagaacaaa ccggcttatt gtagtggaag attttggaga agaatggttt tttggcgatg 490  
agaatgaggg ccaaccaaca gtagggactt aatggccagt ataactaagc ttcagagaca 550  
aagtaaatat ttcaggcatc ctactacttt atcacttcac acagatgaaa tatatttgag 610

<210> 81  
<211> 134  
<212> PRT  
<213> Canis familiaris

<400> 81  
Met Arg Met Leu Leu Asn Leu Ser Leu Leu Ala Leu Gly Ala Ala Tyr  
1 5 10 15

Val Ser Ala Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu  
20 25 30

Thr Leu Thr Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly  
35 40 45

Asn Leu Met Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile  
50 55 60

Lys Glu Val Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His  
65 70 75 80

Gly Glu Ala Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu  
85 90 95

His Ile Glu Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val  
100 105 110

Thr Lys Phe Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr  
115 120 125

Glu Trp Thr Pro Glu Ser  
130

<210> 82  
<211> 610  
<212> DNA  
<213> Canis familiaris

<400> 82

ctcaaatata tttcatctgt gtgaagtgat aaagtagtag gatgcctgaa atatttactt 60  
 tgtctctgaa gcttagttat actggccatt aagtccttac tgttggttgg ccctcattct 120  
 catcgccaaa aaaccattct tctccaaaat ctccactac aataagccgg tttgttctca 180  
 actttccggg gtccactcgg tgtttattac accaagaaat acttgcaggt agtctaggaa 240  
 ctttgtcact ctccatcttt ctctgcaca cttttttttt tggcgctcta tgtgttcttt 300  
 tattaagac aagttttgga atagtttata cacagcctcc ccgtgggcag tttggttctt 360  
 caatgtgtct ataccctgaa aaacttcttt aatgcacagt tgggtgatttt tattttcagg 420  
 agtaggaatc atcaggttcc catcgccat cagccaagtt cgatgagtgg agagcagtgt 480  
 caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 540  
 agccccaaga gctagcaaac tcaaattcag aagcattctc atagctctga aatgttcagt 600  
 gtttgcccttg 610

<210> 83

<211> 402

<212> DNA

<213> Canis familiaris

<400> 83

atgagaatgc ttctgaattt gagtttgcta gctcttgggg ctgcctatgt ttctgccttt 60  
 gctgtagaaa atcccatgaa tagactggtg gcagagacct tgacactgct ctccactcat 120  
 cgaacttggc tgataggcga tgggaacctg atgattccta ctctgaaaa taaaaatcac 180  
 caactgtgca ttaaagaagt ttttcagggt atagacacat tgaagaacca aactgcccac 240  
 ggggaggctg tggataaaact attccaaaac ttgtctttta taaaagaaca catagagcgc 300  
 caaaaaaaaaa ggtgtgcagg agaaagatgg agagtgcaca agttcctaga ctacctgcaa 360  
 gtatttcttg gtgtaataaa caccgagtgg acaccggaaa gt 402

<210> 84

<211> 402



<212> DNA

<213> Canis familiaris

<400> 84

actttccggt gtccactcgg tgttttattac accaagaaat acttgcaggt agtctaggaa 60  
ctttgtcact ctccatcttt ctctgcaca cctttttttt tggcgctcta tgtgttcttt 120  
tattaaagac aagttttgga atagttttatc cacagcctcc ccgtgggcag tttggttctt 180  
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tggtgatttt tattttcagg 240  
agtaggaatc atcaggttcc catcgcttat cagccaagtt cgatgagtgg agagcagtgt 300  
caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 360  
agccccaaga gctagcaaac tcaaattcag aagcattctc at 402

<210> 85

<211> 345

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(345)

<400> 85

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Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr  
1 5 10 15  
ctg ctc tcc act cat cga act tgg ctg ata ggc gat ggg aac ctg atg 96  
Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met  
20 25 30  
att cct act cct gaa aat aaa aat cac caa ctg tgc att aaa gaa gtt 144  
Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val  
35 40 45  
ttt cag ggt ata gac aca ttg aag aac caa act gcc cac ggg gag gct 192  
Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala  
50 55 60  
gtg gat aaa cta ttc caa aac ttg tct tta ata aaa gaa cac ata gag 240  
Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu  
65 70 75 80

cgc caa aaa aaa agg tgt gca gga gaa aga tgg aga gtg aca aag ttc 288  
 Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe  
                     85                    90                    95

cta gac tac ctg caa gta ttt ctt ggt gta ata aac acc gag tgg aca 336  
 Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr  
                     100                    105                    110

ccg gaa agt 345  
 Pro Glu Ser  
             115

<210> 86  
 <211> 115  
 <212> PRT  
 <213> Canis familiaris

<400> 86  
 Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr  
     1                    5                    10                    15

Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met  
                     20                    25                    30

Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val  
                     35                    40                    45

Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala  
                     50                    55                    60

Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu  
                     65                    70                    75                    80

Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe  
                     85                    90                    95

Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr  
                     100                    105                    110

Pro Glu Ser  
             115

<210> 87  
 <211> 345  
 <212> DNA

<213> Canis familiaris

<400> 87

actttccggt gtccactcgg tgtttattac accaagaaat acttgcaggt agtctaggaa 60  
ctttgtcact ctccatcttt ctccctgcaca cctttttttt tggcgctcta tgtgttcttt 120  
tattaaagac aagttttgga atagtttatc cacagcctcc ccgtgggcag tttggttctt 180  
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tgggtgatttt tattttcagg 240  
agtaggaatc atcaggttcc catcgcctat cagccaagtt cgatgagtgg agagcagtgt 300  
caaggtctct gccaccagtc tattcatggg attttctaca gcaaa 345

<210> 88

<211> 166

<212> DNA

<213> Canis familiaris

<400> 88

ctcagcttag gccagcctac gacctgcctg ctcttccctc gtcctcctg cattggctct 60  
gggctccatg gcgctctggt tgactgtggt cattgctctc acctgcctcg gtggccttgc 120  
ctccccgagc cctgtgactc cctccccaac cctcaaggag ctcat 166

<210> 89

<211> 272

<212> DNA

<213> Canis familiaris

<400> 89

tggccttgcc tccccgagcc ctgtgactcc ctccccaacc ctcaaggagc tcattgagga 60  
gctggtcaac atcaccaga atcaggcatc cctctgcaac ggcagcatgg tgtggagcgt 120  
caacctgacc gccggcatgt actgcgcagc tctagaatct ctgatcaatg tctccgactg 180  
cagcgccatc caaaggaccc agaggatgct gaaagcactg tgctctcaaa agcccgcggc 240  
agggcagatt tccagtgaac gcagccgaga ca 272

<210> 90

<211> 278

<212> DNA

<213> Canis familiaris

<400> 90

atggcgctct ggttgactgt ggtcattgct ctcacctgcc tcggtggcct tgcctccccg 60  
agccctgtga ctccctcccc aacctcaag gagctcattg aggagctggt caacatcacc 120  
cagaatcagg catccctctg caacggcagc atggtgtgga gcgtaaacct gaccgccggc 180  
atgtactgcg cagctctaga atctctgac aatgtctccg actgcagcgc catccaaagg 240  
accagagga tgctgaaagc actgtgctct caaaagcc 278

<210> 91

<211> 1302

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (52)..(444)

<400> 91

ctacgacctg cctgctcttc cctgctcct cctgcattgg ctctgggctc c atg gcg 57  
Met Ala  
1  
ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt gcc 105  
Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu Ala  
5 10 15  
tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag 153  
Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu  
20 25 30  
gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc 201  
Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser  
35 40 45 50  
atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta 249  
Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu  
55 60 65  
gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag 297  
Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln  
70 75 80

agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att 345  
 Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile  
           85                          90                          95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 393  
 Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val  
       100                          105                          110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 441  
 Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe  
 115                          120                          125                          130

aga tgaagcatga aaacttagca tccttatctg tagaccacaga cctgaccact 494  
 Arg

taagttccag attcattttt ctttccgacg tcacaaattt cttagggagg tggggggggg 554

ggagaacccat ttcttcagct gggacctcag cctgcaccgc ctgcctccat ggagctgagc 614

ccagccaccc ctgccttggg gcatggggcc cagccgggtg gccctcctcc gtctgcactt 674

catcaacgct gagggaaagc actgcatccc atgactgtcc cctcctcaga gcaaagtgca 734

gcattacagt ggaggcagat atgtgtggga ggggggtcttg ctgtacctgg gagtggcaca 794

gacatgtttc ttcttagcct tatttattat tgtgtgttat ttaaacaagt gtctttgttt 854

gtgctgggga cagggagtgg cttggagctg ggggccaggt gactcgggtt tagagagtcc 914

ctgggaataa gcactgtgtg taaaattctg ctacctcact gggatcctgg ggccgacaca 974

ggggacagga gaaaggggtca gagatgctgc tcttgtctgc cactcagcag ctggccctca 1034

gccaagcagt aatttattgt ttttccttgt atttaaagtt aagaaataaa atatgttatc 1094

aaagagttaa taatatatag aagagtagcc taaaaggctg catttggtgt gtgtggccag 1154

gccggggcgg gtggggggga ggggtgtgtc actgaatgtg ctctttcact gactttgtca 1214

aactggaagc cagaaataaa gatggtgaca agagaaaaaa aaaaaaaaaa aaaaaaaaaa 1274

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1302

<210> 92  
 <211> 131  
 <212> PRT

<213> Canis familiaris

<400> 92

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly  
1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu  
20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn  
35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala  
50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg  
65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly  
85 90 95

Gln Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln  
100 105 110

Leu Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly  
115 120 125

Asn Phe Arg  
130

<210> 93

<211> 1302

<212> DNA

<213> Canis familiaris

<400> 93

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt ttttctcttg 60

tcaccatctt tatttctggc ttccagtttg acaaagtcag tgaaagagca cattcagtga 120

caacaccctc cccccaccc gccccggcct ggccacacac accaaatgca gccttttagg 180

ctactcttct atatattatt aactctttga taacatattt tatttcttaa ctttaaatac 240

aaggaaaaac aataaattac tgcttggttg agggccagct gctgagtggc agacaagagc 300

agcatctctg accctttctc ctgtcccctg tgtcggcccc aggatcccag tgaggtagca 360

gaattttaca cacagtgtt attcccaggg actctctaaa cccgagtcac tgggccccca 420  
 gctccaagcc actccctgtc cccagcacaa acaaagacac ttgtttaaat aacacacaat 480  
 aataaataag gctaagaaga aacatgtctg tgccactccc aggtacagca agacccccctc 540  
 ccacacatat ctgcctccac tgtaatgtct cactttgtct tgaggagggg acagtcattg 600  
 gatgcagtgc tttccctcag cgttgatgaa gtgcagacgg aggagggcca cccggctggg 660  
 ccccatgcac caaggcaggg gtggctgggc tcagctccat ggaggcaggc ggtgcaggct 720  
 gaggtcccag ctgaggaaat ggttctcccc cccccccacc tccctaagaa atttgtgacg 780  
 tcggaaagaa aatgaatct ggaacttaag tggtcaggct tgggtctaca gataaggatg 840  
 ctaagttttc atgtttcatc tgaaatttcc atggcgataa actcccctta cataggtgag 900  
 caggtttttc accaactgga tcacttcaat tttggtgtct cggctgcgtt cactggaaat 960  
 ctgccctgcc gggggctttt gagagcacag tgctttcagc atcctctggg tcctttggat 1020  
 ggcgctgcag tcggagacat tgatcagaga ttctagagct gcgcagtaca tgccggcggt 1080  
 caggttgacg ctccacacca tgctgccgtt gcagagggat gcctgattct gggatgatgtt 1140  
 gaccagctcc tcaatgagct ccttgagggt tggggagggg gtcacagggc tcggggaggc 1200  
 aaggccaccg aggcagggtg gagcaatgac cacagtcaac cagagcgcca tggagcccag 1260  
 agccaatgca ggaggagcga gggaagagca ggcaggctgt ag 1302

<210> 94  
 <211> 393  
 <212> DNA  
 <213> Canis familiaris

<400> 94  
 atggcgctct ggttgactgt ggtcattgct ctacactgcc tcggtggcct tgctccccg 60  
 agccctgtga ctccctcccc aacctcaag gagctcattg aggagctggc caacatcacc 120  
 cagaatcagg catccctctg caacggcagc atggtgtgga gcgtcaacct gaccgccggc 180  
 atgtactgcg cagctctaga atctctgatc aatgtctccg actgcagcgc catccaaagg 240

accagagga tgctgaaagc actgtgctct caaaagcccg cggcagggca gatttccagt 300  
gaacgcagcc gagacaccaa aattgaagtg atccagttgg tgaaaaacct gctcacctat 360  
gtaaggggag tttatcgcca tggaaatttc aga 393

<210> 95  
<211> 393  
<212> DNA  
<213> Canis familiaris

<400> 95  
tctgaaattt ccatggcgat aaactcccct tacataggtg agcagggttt tcaccaactg 60  
gatcacttca attttggtgt ctcggtgctg ttcactggaa atctgccctg ccgcgggctt 120  
ttgagagcac agtgctttca gcatcctctg ggtcctttgg atggcgctgc agtcggagac 180  
attgatcaga gattctagag ctgcgcagta catgccggcg gtcagggtga cgctccacac 240  
catgctgccg ttgcagaggg atgcctgatt ctgggtgatg ttgaccagct cctcaatgag 300  
ctccttgagg gttggggagg gagtcacagg gctcggggag gcaaggccac cgaggcaggt 360  
gagagcaatg accacagtca accagagcgc cat 393

<210> 96  
<211> 333  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (1)..(333)

<400> 96  
agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag gag ctg 48  
Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu  
1 5 10 15  
gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96  
Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val  
20 25 30  
tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144  
Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser



35

40

45

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192  
 Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met  
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att tcc agt 240  
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser  
 65 70 75 80

gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac 288  
 Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn  
 85 90 95

ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 333  
 Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg  
 100 105 110

&lt;210&gt; 97

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Canis familiaris

&lt;400&gt; 97

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu  
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val  
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser  
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met  
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser  
 65 70 75 80

Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn  
 85 90 95

Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg  
 100 105 110

&lt;210&gt; 98

25!

<211> 333  
 <212> DNA  
 <213> Canis familiaris

<400> 98  
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 gatcacttca attttggtgt ctcggtgcg ttactggaa atctgccctg ccgcgggctt 120  
 ttgagagcac agtgctttca gcatcctctg ggctccttgg atggcgctgc agtcggagac 180  
 attgatcaga gattctagag ctgcgcagta catgccggcg gtcagggttga cgctccacac 240  
 catgctgccg ttgcagaggg atgctgatt ctgggtgatg ttgaccagct cctcaatgag 300  
 ctcttgagg gttggggagg gagtcacagg gct 333

<210> 99  
 <211> 1269  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (57)..(446)

<400> 99  
 ccagcctacg acctgcctgc tcttccctcg ctctcctgc attggtctg ggtcc atg 59  
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 Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu  
 5 10 15  
 gcc tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att 155  
 Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile  
 20 25 30  
 gag gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc 203  
 Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly  
 35 40 45  
 agc atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct 251  
 Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala  
 50 55 60 65

cta gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc 299  
 Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr  
                     70                    75                    80

cag agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att 347  
 Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile  
                     85                    90                    95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 395  
 Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val  
                     100                    105                    110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 443  
 Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe  
                     115                    120                    125

aga tgaagcatga aaacttagca tccttatctg tagaccacaga cctgaccact 496  
 Arg  
 130

taagttccag attcattttt ctttccgacg tcacaaattt cttagggagg tggggggggg 556

ggagaaccat ttctcagct gggacctcag cctgcaccgc ctgcctccat ggagctgagc 616

ccagccaccc ctgccttggt gcatggggcc cagccgggtg gccctcctcc gtctgcactt 676

catcaacgct gagggaaagc actgcatccc atgactgtcc cctcctcaga gcaaagtgca 736

gcattacagt ggaggcagat atgtgtggga ggggtcttg ctgtacctgg gagtggcaca 796

gacatgtttc ttcttagcct tatttattat tgtgtgttat ttaaacaagt gtctttgttt 856

gtgctgggga caggagtggt cttggagctg ggggccaggt gactcgggtt tagagagtcc 916

ctgggaataa gactgtgtg taaaattctg ctacctcact gggatcctgg ggccgacaca 976

ggggacagga gaaaggggtca gagatgctgc tcttgtctgc cactcagcag ctggccctca 1036

gccaagcagt aatttattgt ttttccttgt atttaaagtt aagaaataaa atatgttatc 1096

aaagagttaa taatatatag aagagtagcc taaaaggctg catttggtgt gtgtggccag 1156

gccggggcgg gtggggggga ggggtgtgtc actgaatgtg ctctttcact gactttgtca 1216

aactggaagc cagaaataaa gatggtgaca agagaaaaaa aaaaaaaaaa aaa 1269

<210> 100

<211> 130  
 <212> PRT  
 <213> Canis familiaris

<400> 100

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly  
 1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu  
 20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn  
 35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala  
 50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg  
 65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly  
 85 90 95

Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu  
 100 105 110

Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn  
 115 120 125

Phe Arg  
 130

<210> 101  
 <211> 1269  
 <212> DNA  
 <213> Canis familiaris

<400> 101

tttttttttt tttttttttt tcttgtcacc atctttatct ctggcttcca gtttgacaaa 60  
 gtcagtgaag gagcacattc agtgacaaca ccttcccccc caccgcgccg ggcttgagcca 120  
 cacacaccaa atgcagcctt ttaggctact cttctatata ttattaactc tttgataaca 180  
 tattttatct cttaacttta aatacaagga aaaacaataa attactgctt ggctgagggc 240  
 cagctgctga gtggcagaca agagcagcat ctctgaccct ttctcctgtc cctgtgtctg 300

607036: 1269-1270

gccccaggat ccagtgagg tagcagaatt ttacacacag tgcttattcc cagggactct 360  
 ctaaaccgga gtcactgggc cccagctcc aagccactcc ctgtccccag cacaaacaaa 420  
 gacacttggt taaataacac acaataataa ataaggctaa gaagaaacat gtctgtgcca 480  
 ctcccaggta cagcaagacc ccctcccaca catatctgcc tccactgtaa tgctgcactt 540  
 tgctctgagg aggggacagt catgggatgc agtgctttcc ctcagcgttg atgaagtgca 600  
 gacggaggag ggccaccggt ctgggccccca tgcaccaagg caggggtggc tgggctcagc 660  
 tccatggagg caggcgggtgc aggtcaggt cccagctgag gaaatgggtc tcccccccc 720  
 ccacctccct aagaaatttg tgacgtcgga aagaaaaatg aatctggaac ttaagtggtc 780  
 aggtctgggt ctacagataa ggatgctaag ttttcacgtc tcactgaaa tttccatggc 840  
 gataaactcc ccttacatag gtgagcaggt ttttcaccaa ctggatcact tcaatttttg 900  
 tgtctcggct gcgttcactg gaaatccctg ccgcgggctt ttgagagcac agtgctttca 960  
 gcatcctctg ggctcctttg atggcgctgc agtcggagac attgatcaga gattctagag 1020  
 ctgcgcagta catgccggcg gtcagggtga cgctccacac catgctgccg ttgcagaggg 1080  
 atgcctgatt ctgggtgatg ttgaccagct cctcaatgag ctccctgagg gttggggagg 1140  
 gagtcacagg gctcggggag gcaaggccac cgaggcaggt gagagcaatg accacagtca 1200  
 accagagcgc catggagccc agagccaatg caggaggagc gagggaagag caggcaggtc 1260  
 gtaggctgg 1269

<210> 102  
 <211> 390  
 <212> DNA  
 <213> Canis familiaris

<400> 102  
 atggcgctct ggttgactgt ggtcattgct ctacactgcc tcggtggcct tgcctccccg 60  
 agccctgtga ctccctcccc aaccctcaag gagctcattg aggagctggt caacatcacc 120  
 cagaatcagg catccctctg caacggcagc atgggtgtgga gcgtcaacct gaccgcccgc 180

atgtactgcg cagctctaga atctctgac aatgtctccg actgcagcgc catccaaagg 240  
 acccagagga tgctgaaagc actgtgctct caaaagccccg cggcagggat ttccagtga 300  
 cgcagccgag acacaaaaat tgaagtgatc cagttgggtga aaaacctgct cacctatgta 360  
 aggggagttt atcgccatgg aaatttcaga 390

<210> 103  
 <211> 390  
 <212> DNA  
 <213> Canis familiaris

<400> 103  
 tctgaaattt ccatggcgat aaactcccct tacataggtg agcaggtttt tcaccaactg 60  
 gatcacttca attttgggtgt ctcggctgcg ttcactggaa atccctgccg cgggcttttg 120  
 agagcacagt gctttcagca tcctctgggt cctttggatg gcgctgcagt cggagacatt 180  
 gatcagagat tctagagctg cgcagtacat gccggcggtc aggttgacgc tccacaccat 240  
 gctgccgttg cagaggggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300  
 cttgaggggtt ggggagggag tcacagggct cggggaggca aggccaccga ggcaggtgag 360  
 agcaatgacc acagtcaacc agagcgccat 390

<210> 104  
 <211> 330  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(330)

<400> 104  
 agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag gag ctg 48  
 Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu  
 1 5 10 15  
 gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96  
 Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val  
 20 25 30

tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144  
 Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser  
           35                    40                    45

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192  
 Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met  
           50                    55                    60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att tcc agt gaa 240  
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu  
           65                    70                    75                    80

cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac ctg 288  
 Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu  
                     85                    90                    95

ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 330  
 Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg  
                     100                    105                    110

<210> 105  
 <211> 110  
 <212> PRT  
 <213> Canis familiaris

<400> 105  
 Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu  
   1                    5                    10                    15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val  
                     20                    25                    30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser  
           35                    40                    45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met  
           50                    55                    60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu  
           65                    70                    75                    80

Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu  
                     85                    90                    95

Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg  
           100                    105                    110

257

Sequence: CEF00000

<210> 106  
 <211> 330  
 <212> DNA  
 <213> Canis familiaris

<400> 106  
 tctgaaat t t ccatggcgat aaactcccct tacataggtg agcagggttt tcaccaactg 60  
 gatcacttca attttggtgt ctcggtgcg t t cactggaa atccctgccg cgggcttttg 120  
 agagcacagt gctttcagca t c t c t g g g t c c t t t g g a t g g c g c t g c a g t c g g a g a c a t t 180  
 gatcagagat tctagagctg cgcagtacat gccggcggtc aggttgacgc tccacaccat 240  
 gctgccgttg cagagggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300  
 cttgagggtt ggggaggag t c a c a g g g c t 330

<210> 107  
 <211> 567  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(567)

<400> 107  
 atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48  
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
 1 5 10 15  
 aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96  
 Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
 20 25 30  
 ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144  
 Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
 35 40 45  
 gcc agc tcc tgt cag aag gac aga aat gac ttc gcc ttc ccc cag gac 192  
 Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
 50 55 60  
 gtg ttt ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg 240  
 Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val

258



65	70	75	80	
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc				288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser				
	85	90	95	
tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga				336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly				
	100	105	110	
ctt gat tgg cag ctg acc cgc ctg gaa gcc tgt gtc atg cag gag gtg				384
Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val				
	115	120	125	
ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac				432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn				
	130	135	140	
tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct				480
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro				
	145	150	155	160
tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat				528
Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr				
	165	170	175	
tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa				567
Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys				
	180	185		
<210> 108				
<211> 189				
<212> PRT				
<213> Felis catus				
<400> 108				
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys				
1	5	10	15	
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu				
	20	25	30	
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro				
	35	40	45	
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp				
	50	55	60	

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val  
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn  
130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro  
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr  
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
180 185

<210> 109

<211> 567

<212> DNA

<213> Felis catus

<400> 109

tttctcgtc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180

ccccacctcc tgcattgacac aggtctccag gcgggtcagc tgccaatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360

gtctccacca aacacgtcct gggggaaggc gaagtcattt ctgtccttct gacaggagct 420

ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480

gggtctgagggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540

caccaagaag gaagagggca gcgccat 567

<210> 110

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 110

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48  
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
1 5 10 15

aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96  
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144  
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
35 40 45

gcc agc tcc tgt cag aag gac agg aat gac ttc gcc ttc ccc cag gac 192  
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
50 55 60

gtg ttc ggt gga gac cag tcc cac aag gct caa gcc ctc tcg gtg gtg 240  
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

cac gtg acg aac cag gag atc ttc cac ttc ttc tgc aca gag gcg tcc 288  
His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336  
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg 384  
Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val  
115 120 125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc ctc ctg agg aac 432

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn  
 130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480  
 Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro  
 145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528  
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr  
 165 170 175

tca tca aca gcc ttg caa aaa aga tta agg agc gag aaa 567  
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
 180 185

<210> 111  
 <211> 189  
 <212> PRT  
 <213> Felis catus

<400> 111  
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
 1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
 20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
 35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
 50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
 65 70 75 80

His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
 85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
 100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val  
 115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn  
 130 135 140

262

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro  
 145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr  
 165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
 180 185

<210> 112  
 <211> 567  
 <212> DNA  
 <213> Felis catus

<400> 112  
 tttctcgtc cttaatcttt ttgcaaggc tgttgatgaa taatacaagg atctcatgat 60  
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120  
 gagtctttgg aagtagttcc tcaggaggga gtccctggtc gtgaggggag cctctccctc 180  
 cccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240  
 gaattcctcc aggaggggtg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300  
 gtggaagatc tcctggttcg tcacgtgcac caccgagagg gcttgagcct tgtgggactg 360  
 gtctccaccg aacacgtcct gggggaaggc gaagtcattc ctgtccttct gacaggagct 420  
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480  
 ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540  
 caccaagaag gaagagggca gcgccat 567

<210> 113  
 <211> 498  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1) .. (498)

<400> 113

tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg	48
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr	
1 5 10 15	
ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac	96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp	
20 25 30	
aga aat gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc	144
Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser	
35 40 45	
cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc	192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile	
50 55 60	
ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc	240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr	
65 70 75 80	
acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc	288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg	
85 90 95	
ctg gaa gcc tgt gtc atg cag gag gtg ggg gag gga gag gct ccc ctc	336
Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu	
100 105 110	
acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc	384
Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu	
115 120 125	
tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga	432
Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg	
130 135 140	
gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa	480
Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys	
145 150 155 160	
aga tta agg agc gag aaa	498
Arg Leu Arg Ser Glu Lys	
165	

<210> 114  
 <211> 166  
 <212> PRT

<213> Felis catus

<400> 114

Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile  
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr  
65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg  
85 90 95

Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu  
115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg  
130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys  
145 150 155 160

Arg Leu Arg Ser Glu Lys  
165

<210> 115

<211> 498

<212> DNA

<213> Felis catus

<400> 115

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180

265

cccacacctcc tgcacgacac aggcctccag gcgggtcagc tgccaatcaa gtcccgtgca 240  
 gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300  
 gtggaagatc ttctgggtcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360  
 gtctccacca aacacgtcct gggggaaggc gaagtcattt ctgtccttct gacaggagct 420  
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480  
 ggtctgaggc aggtcaca 498

<210> 116  
 <211> 498  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(498)

<400> 116  
 tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48  
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
 1 5 10 15  
 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96  
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
 20 25 30  
 agg aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144  
 Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
 35 40 45  
 cac aag gct caa gcc ctc tcg gtg gtg cac gtg acg aac cag gag atc 192  
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile  
 50 55 60  
 ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240  
 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ala Ala Trp Asn Thr  
 65 70 75 80  
 acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc 288  
 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg  
 85 90 95

206



ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctc 336  
 Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
                   100                                  105                                  110

acg aac gag gac tcc ctc ctg agg aac tac ttc caa aga ctc tcc ctc 384  
 Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu  
                   115                                  120                                  125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432  
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg  
                   130                                  135                                  140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg caa aaa 480  
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys  
 145                                  150                                  155                                  160

aga tta agg agc gag aaa 498  
 Arg Leu Arg Ser Glu Lys  
                                   165

<210> 117  
 <211> 166  
 <212> PRT  
 <213> Felis catus

<400> 117  
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
           1                                  5                                  10                                  15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
                   20                                  25                                  30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
                   35                                  40                                  45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile  
           50                                  55                                  60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr  
           65                                  70                                  75                                  80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg  
                   85                                  90                                  95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
                   100                                  105                                  110

Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu  
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg  
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys  
 145 150 155 160

Arg Leu Arg Ser Glu Lys  
 165

<210> 118  
 <211> 498  
 <212> DNA  
 <213> Felis catus

<400> 118  
 tttctcgctc cttaatcttt ttgcaaggc tgttgatgaa taatacaagg atctcatgat 60  
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120  
 gagtctttgg aagtagttcc tcaggaggga gtcctcgttc gtgaggggag cctctccctc 180  
 cccacctcc tgcacgacac aggttccag gcgggtcagc tgccgatcaa gtcccgtgca 240  
 gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300  
 gtggaagate tcctggttcg tcacgtgcac caccgagagg gcttgagcct tgtgggactg 360  
 gtctccaccg aacacgtcct gggggaaggc gaagtcattc ctgtccttct gacaggagct 420  
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480  
 ggtctgaggc aggtcaca 498

<210> 119  
 <211> 444  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (10)..(441)

<400> 119

ggatccacc atg tgg ctg cag aac ctg ctt ttc ctg ggc act gtg gtc tgc 51  
 Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys  
 1 5 10

agc atc tct gca ccc acc agt tca ccc agc tct gtc act cgg ccc tgg 99  
 Ser Ile Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp  
 15 20 25 30

caa cac gtg gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt 147  
 Gln His Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser  
 35 40 45

agt gaa ata act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa 195  
 Ser Glu Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu  
 50 55 60

atg ttt gac cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg 243  
 Met Phe Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu  
 65 70 75

tac gag cag ggc cta cgg ggc agc ctc atc agc ctc aag gag cct ctg 291  
 Tyr Glu Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu  
 80 85 90

aga atg atg gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa 339  
 Arg Met Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu  
 95 100 105 110

acg ccc tgt gaa acc cag act atc acc ttc aaa aat ttc aaa gag aat 387  
 Thr Pro Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn  
 115 120 125

ctg aag gat ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac 435  
 Leu Lys Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp  
 130 135 140

cag aag taa 444  
 Gln Lys

<210> 120  
 <211> 144  
 <212> PRT  
 <213> Felis catus

<400> 120  
 Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys Ser Ile  
 1 5 10 15

269

CCCTGTTT = 433T9460

Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His  
20 25 30

Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu  
35 40 45

Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe  
50 55 60

Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu  
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met  
85 90 95

Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro  
100 105 110

Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys  
115 120 125

Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys  
130 135 140

<210> 121

<211> 444

<212> DNA

<213> Felis catus

<400> 121

ttactttctgg tctggtcccc agcagtc aaa ggggttgta aacagaaaat ccttcagatt 60

ctctttgaaa tttttgaagg tgatagtctg ggtttcacag ggcgtttccg gagtaagggg 120

gcagtgtctgc ttgtaatggt tggccatcat tctcagaggc tccttgaggc tgatgaggct 180

gccccgtagg cctgtctgt acagcttttag gtgagtctgc aggcatttcg gtcctcagg 240

gtcaaacatt tcagagacga cttctactgc ttcattcatc acagcagtta tttcactact 300

gttgttcaga aggctcaggg cctccttgat ggcattccacg tggttgccagg gccgagtgc 360

agagctgggt gaactggtgg gtgcagagat gctgcagacc acagtgccca ggaaaagcag 420

gttctgcagc cacatggtgg atcc 444

<210> 122  
<211> 432  
<212> DNA  
<213> Felis catus

<400> 122  
atgtggctgc agaacctgct tttcctgggc actgtggtct gcagcatctc tgcacccacc 60  
agttcaccca gctctgtcac tcggccctgg caacacgtgg atgccatcaa ggaggccctg 120  
agccttctga acaacagtag tgaaataact gctgtgatga atgaagcagt agaagtcgtc 180  
tctgaaatgt ttgacctga ggagccgaaa tgcctgcaga ctcacctaaa gctgtacgag 240  
cagggcctac ggggcagcct catcagcctc aaggagcctc tgagaatgat ggccaaccat 300  
tacaagcagc actgccccct tactccggaa acgccctgtg aaaccagac tatcaccttc 360  
aaaaatttca aagagaatct gaaggatttt ctgtttaaca acccctttga ctgctgggga 420  
ccagaccaga ag 432

<210> 123  
<211> 432  
<212> DNA  
<213> Felis catus

<400> 123  
cttctggtct ggtccccagc agtcaaaggg gttgttaaac agaaaatcct tcagattctc 60  
tttgaaattt ttgaaggtga tagtctgggt ttcacagggc gtttccggag taagggggca 120  
gtgctgcttg taatggttgg ccatcattct cagaggctcc ttgaggctga tgaggctgcc 180  
ccgtaggccc tgctcgtaca gctttaggtg agtctgcagg catttcggct cctcagggtc 240  
aaacatttca gagacgactt ctactgcttc attcatcaca gcagttattt cactactgtt 300  
gttcagaagg ctcagggcct ccttgatggc atccacgtgt tgccagggcc gagtgacaga 360  
gctgggtgaa ctggtgggtg cagagatgct gcagaccaca gtgccagga aaagcaggtt 420  
ctgcagccac at 432

<210> 124

<211> 381  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(381)

<400> 124

gca ccc acc agt tca ccc agc tct gtc act cgg ccc tgg caa cac gtg 48  
 Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val  
 1 5 10 15

gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt agt gaa ata 96  
 Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile  
 20 25 30

act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa atg ttt gac 144  
 Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp  
 35 40 45

cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg tac gag cag 192  
 Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln  
 50 55 60

ggc cta cgg ggc agc ctc atc agc ctc aag gag cct ctg aga atg atg 240  
 Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met  
 65 70 75 80

gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa acg ccc tgt 288  
 Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys  
 85 90 95

gaa acc cag act atc acc ttc aaa aat ttc aaa gag aat ctg aag gat 336  
 Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp  
 100 105 110

ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac cag aag 381  
 Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys  
 115 120 125

<210> 125  
 <211> 127  
 <212> PRT  
 <213> Felis catus

<400> 125

Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val  
1 5 10 15

Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile  
20 25 30

Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp  
35 40 45

Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln  
50 55 60

Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met  
65 70 75 80

Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys  
85 90 95

Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp  
100 105 110

Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys  
115 120 125

<210> 126

<211> 381

<212> DNA

<213> Felis catus

<400> 126

cttctggtct ggtccccagc agtcaaaggg gttgttaaac agaaaatcct tcagattctc 60

tttgaaattt ttgaaggtga tagtctgggt ttcacagggc gtttccggag taagggggca 120

gtgctgcttg taatgggttg ccatcattct cagaggtcc ttgaggtga tgaggtgcc 180

ccgtaggccc tgctcgtaca gctttaggtg agtctgcagg catttcggct cctcagggtc 240

aaacatttca gagacgactt ctactgcttc attcatcaca gcagttattt cactactgtt 300

gttcagaagg ctcaaggcct ccttgatggc atccacgtgt tgccagggcc gagtgacaga 360

gctgggtgaa ctggtgggtg c 381

<210> 127

<211> 28





<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 131  
ctgttcagag tttgagtaag cc

22

<210> 132  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 132  
gaagatacca tttcaacttt aacacagc

28

<210> 133  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 133  
tgctgtattg tgaagactcc cagc

24

<210> 134  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 134  
atgcactttc tttgcc

16

<210> 135  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 135  
ctggaggaaa akacttcrat gattctgata tctgaaatat at 42

<210> 136  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 136  
ctgacycttk sttggscttc attctca 27

<210> 137  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 137  
gggctcgaga aaagatttgc tgtagaaaat cccatg 36

<210> 138  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

Primer

<400> 138  
cccgcggccg ctcaactttc cgggtgtccac tc 32

<210> 139  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 139  
gtcmtggctc tyrcttgcc tgg 23

<210> 140  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 140  
aaastgggcy acytcgattt tgg 23

<210> 141  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 141  
gtgatgttg yacagtcctc 20

<210> 142  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 142

aattaaccct cactaaaggg

20

<210> 143

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 143

atggcgctct ggttgactgt

20

<210> 144

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 144

ggcttttgag agcacagtgc

20

<210> 145

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 145

ccccatatga gccctgtgac tccctcccc

29

<210> 146  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 146  
ggggaattct catctgaaat ttccatggcg

30

<210> 147  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 147  
atggcgctgc cctcttcctt cttg

24

<210> 148  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 148  
tcatttctcg ctccttaatc ttttctgc

28

<210> 149  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 149  
cagggatcca ccatgtggct gcagaacctg cttttcc

37

<210> 150  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 150  
ttacttctgg tctggcccc agcagtcaaa ggggttgta aacagaaaat

50

<210> 151  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 151  
cacagyccca tctcctcc

18

<210> 152  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 152  
gtaatacgac tcactatagg gc

22

<210> 153  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 153

acggaattcg agatgatagt gctggc

26

<210> 154

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 154

gtgtctagat ttggtagaaa aggatgat

28

<210> 155

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 155

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48  
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
1 5 10 15

aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96  
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144  
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
35 40 45

gcc agc tcc tgt cag aag gac aga agt gac ttc gcc ttc ccc cag gac 192  
Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp  
50 55 60

gtg ttt ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg 240  
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc 288  
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336  
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

ctt gat tgg cag ctg acc cgc ctg gaa gcc tgt gtc atg cag gag gtg 384  
Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val  
115 120 125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac 432  
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn  
130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480  
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro  
145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528  
Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr  
165 170 175

tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa 567  
Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
180 185

<210> 156  
<211> 189  
<212> PRT  
<213> Felis catus

<400> 156  
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
35 40 45



Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp  
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val  
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn  
130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro  
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr  
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
180 185

<210> 157  
<211> 567  
<212> DNA  
<213> Felis catus

<400> 157

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180

ccccacctcc tgcatgacac aggcttccag gcgggtcagc tgccaatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360

gtctccacca aacacgtcct gggggaaggc gaagtcactt ctgtccttct gacaggagct 420

ggcagggagt ctctcatatt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480  
 ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540  
 caccaagaag gaagagggca gcgccat 567

<210> 158  
 <211> 498  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(498)

<400> 158  
 tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48  
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
 1 5 10 15  
 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96  
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
 20 25 30  
 aga agt gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc 144  
 Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
 35 40 45  
 cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192  
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile  
 50 55 60  
 ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240  
 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr  
 65 70 75 80  
 acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc 288  
 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg  
 85 90 95  
 ctg gaa gcc tgt gtc atg cag gag gtg ggg gag gga gag gct ccc ctc 336  
 Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
 100 105 110  
 acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc 384  
 Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu  
 115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432  
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg  
 130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa 480  
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys  
 145 150 155 160

aga tta agg agc gag aaa 498  
 Arg Leu Arg Ser Glu Lys  
 165

<210> 159  
 <211> 166  
 <212> PRT  
 <213> Felis catus

<400> 159  
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
 1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
 20 25 30

Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile  
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr  
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg  
 85 90 95

Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
 100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu  
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg  
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys

285

145

150

155

160

Arg Leu Arg Ser Glu Lys  
165

&lt;210&gt; 160

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; Felis catus

&lt;400&gt; 160

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtccctcgttc gtgaggggag cctctccctc 180

ccccacctcc tgcattgacac aggcttccag gcgggtcagc tgccaatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360

gtctccacca aacacgtcct gggggaaggc gaagtcactt ctgtccttct gacaggagct 420

ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480

ggctctgaggc aggtcaca 498

&lt;210&gt; 161

&lt;211&gt; 582

&lt;212&gt; DNA

&lt;213&gt; Felis catus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(582)

&lt;400&gt; 161

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys

1

5

10

15

aac tcc gtc tgc tct ctg ggc tgt gat ctg cct cag acc cac ggc ctg 96

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu

20

25

30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct	144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro	
35 40 45	
gcc agc tcc tgt cag aag gac aga agt gac ttc gcc ttc ccc cag gac	192
Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp	
50 55 60	
gtg ttc ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg	240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val	
65 70 75 80	
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc	288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser	
85 90 95	
tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga	336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly	
100 105 110	
ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg	384
Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val	
115 120 125	
ggg gag gga gag gct ccc ctg acg aac gag gac att cat ccc gag gac	432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp	
130 135 140	
tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc tac ctg caa gag	480
Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu	
145 150 155 160	
aag aaa tac agc cct tgt gcc tgg gag atc gtc aga gca gaa atc atg	528
Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met	
165 170 175	
aga tcc ttg tat tat tca tca aca gcc ttg cag aaa aga tta agg agc	576
Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser	
180 185 190	
gag aaa	582
Glu Lys	

<210> 162  
 <211> 194  
 <212> PRT

<213> Felis catus

<400> 162

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp  
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val  
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp  
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu  
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met  
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser  
180 185 190

Glu Lys

<210> 163

<211> 582

<212> DNA

<213> Felis catus

<400> 163

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60  
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120  
 gagtctttgg aagtagttcc tcaggatgga gtcctcgga tgaatgtcct cgttcgtcag 180  
 gggagcctct cctccccca cctcctgcac gacacaggct tccaggcggg tcagctgccg 240  
 atcaagtccc gtgcagaatt cctccaggag ggtggtgttc caagcagcag acgaggacgc 300  
 ctctgtgcag aagaagtgga agatcttctg gttcgtcacg tgcaccaccg agagggttg 360  
 ggccttggtg gactggtctc caccgaacac gtcctggggg aaggcgaagt cacttctgtc 420  
 cttctgacag gagctggcag ggagtctcct catttgctcc aggagcgtca aggccctcct 480  
 gttcagcagg ccgtgggtct gaggcagatc acagcccaga gagcagacgg agttgcagcc 540  
 cagcgccacc agggccacca agaaggaaga gggcagcgcc at 582

<210> 164

<211> 513

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(513)

<400> 164

tgt gat ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48  
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
 1 5 10 15  
 ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96  
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
 20 25 30  
 aga agt gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144  
 Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
 35 40 45  
 cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192  
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile  
 50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240  
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr  
65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc 288  
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg  
85 90 95

ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctg 336  
Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
100 105 110

acg aac gag gac att cat ccc gag gac tcc atc ctg agg aac tac ttc 384  
Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr Phe  
115 120 125

caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct tgt gcc 432  
Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala  
130 135 140

tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat tca tca 480  
Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser  
145 150 155 160

aca gcc ttg cag aaa aga tta agg agc gag aaa 513  
Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
165 170

<210> 165  
<211> 171  
<212> PRT  
<213> Felis catus

<400> 165  
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
20 25 30

Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile  
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr



65

70

75

80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg  
85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
100 105 110

Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr Phe  
115 120 125

Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala  
130 135 140

Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser  
145 150 155 160

Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
165 170

<210> 166

<211> 513

<212> DNA

<213> Felis catus

<400> 166

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtctctggga tgaatgtcct cgttcgtcag 180

gggagcctct cctccccca cctcctgcac gacacaggct tccaggcggg tcagctgccg 240

atcaagtccc gtgcagaatt cctccaggag ggtggtgttc caagcagcag acgaggacgc 300

ctctgtgcag aagaagtgga agatcttctg gtctgtcacg tgcaccaccg agagggcttg 360

ggccttgtagg gactggtctc caccgaacac gtctgtgggg aaggcgaagt cacttctgtc 420

cttctgacag gagctggcag ggagtctcct catttgtccc aggagcgtca aggccctcct 480

gttcagcagg ccgtgggtct gaggcagatc aca 513

<210> 167

<211> 567

<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (1)..(567)

<400> 167

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc	48
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys	
1 5 10 15	
aac tct gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg	96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu	
20 25 30	
ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct	144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro	
35 40 45	
gcc agc tcc tgc cag aag gac aga aat gac ttc gcc ttc ccc cag gac	192
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp	
50 55 60	
gtg ttc ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg	240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val	
65 70 75 80	
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc	288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser	
85 90 95	
tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga	336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly	
100 105 110	
ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg	384
Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val	
115 120 125	
ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac	432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn	
130 135 140	
tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct	480
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro	
145 150 155 160	

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528  
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr  
                   165                  170                  175

tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa 567  
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
                   180                  185

<210> 168  
 <211> 189  
 <212> PRT  
 <213> Felis catus

<400> 168  
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
       1                  5                  10                  15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
                   20                  25                  30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
                   35                  40                  45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
                   50                  55                  60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
       65                  70                  75                  80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
                   85                  90                  95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
                   100                  105                  110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val  
                   115                  120                  125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn  
                   130                  135                  140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro  
       145                  150                  155                  160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr  
                   165                  170                  175

293

664667: 434363

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys  
180 185

<210> 169  
<211> 567  
<212> DNA  
<213> Felis catus

<400> 169  
tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60  
ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120  
gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180  
ccccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240  
gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300  
gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360  
gtctccaccg aacacgtcct gggggaaggc gaagtcattt ctgtccttct ggcaggagct 420  
ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480  
ggctctgaggc aggtcacagc ccagagagca gacagagttg cagcccagcg ccaccagggc 540  
caccaagaag gaagagggca gcgccat 567

<210> 170  
<211> 498  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (1)..(498)

<400> 170  
tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48  
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
1 5 10 15  
ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgc cag aag gac 96  
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp  
20 25 30

aga aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144  
 Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
 35 40 45

cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192  
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile  
 50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240  
 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr  
 65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc 288  
 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg  
 85 90 95

ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctc 336  
 Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
 100 105 110

acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc 384  
 Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu  
 115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432  
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg  
 130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa 480  
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys  
 145 150 155 160

aga tta agg agc gag aaa 498  
 Arg Leu Arg Ser Glu Lys  
 165

<210> 171  
 <211> 166  
 <212> PRT  
 <213> Felis catus

<400> 171  
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr  
 1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp

20

25

30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser  
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile  
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr  
65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg  
85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu  
100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu  
115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg  
130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys  
145 150 155 160

Arg Leu Arg Ser Glu Lys  
165

<210> 172

<211> 498

<212> DNA

<213> Felis catus

<400> 172

tttctcgtc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgttc gtgaggggag cctctccctc 180

ccccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240

gaattcctcc aggagggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtggaagatc ttctggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360

gtctccaccg aacacgtcct gggggaaggc gaagtcattt ctgtccttct ggcaggagct 420  
ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480  
ggtctgaggc aggtcaca 498

<210> 173

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 173

attagatcc atggcgctgc cctcttct

29

<210> 174

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Primer

<400> 174

gcctctagac tgtcatttct cgctccttaa tcttttctgc

40